# FIG. 1A-1

(SEQ ID NO:1)

	(SEC	<b>Q</b> ID !	NO:1	)														
5'	GAG	ACT	11 CAC		CAA	20 GCT	AAG	GCG	29 AAG	AGT	GGG	38 TGG	CTG	AAG	47 CCA	TAC	TAT	56 TTT 
	ATA	GAA	6: TTA		GAA			AAA		3 ATC				GAA				110 AAA
(S	EQ II	ON C	:2) -	» М	E	S	R	K	D	I	T	N	Q	E	E	L	W	K
	ATG	AAG	119 CCT	AGG	AGA	128 AAT		GAA		GAC		146 TAT	TTG	CAT	155 AAG	GAC	ACG	164 GGA
	M	K	P	R	R	N	L	E	E	D	D	Y	L	н	K	D	T	G
	GAG	ACC	173 AGC	ATG	CTA	182 AAA	AGA	ССТ	191 GTG	CTT	TTG	200 CAT	TTG	CAC	209 CAA	ACA	GCC	218 CAT
	E	T	s	M	L	K	R	P	v	L	L	Н	L	Н	Q	T	A	Н
	GCT	GAT	227 GAA		GAC	236 TGC		.TCA				254 CAC		CAG	263 GAA		ттт	272 CCA
	Α	D	Е	F	D	С	P	s	E	L	Q	Н	Т	Q	E	L	F	P
	CAG	TGG	281 CAC	TTG	CCA		AAA	ATA		GCT			GCA			ACT		326 CTT
	Q	W	Ħ	L	P	I	ĸ	I	A	A	I	I	A	S	L	T	F	L
	TAC	ACT	335 CTT	CTG	AGG	344 GAA	GTA	ATT		CCT		362 GCA	ACT	TCC	371 CAT	CAA	CAA	380 TAT
	TAC	ACT  T		CTG L		GAA		ATT  I	CAC		TTA						CAA  Q	
	Y	 T	CTT  L 389	_ <u>L</u>	R .	GAA  E 398			CAC  H.	CCT  P	TTA  L	GCA  A 416	 Т	 s	CAT  H 425	Ω	Q	TAT  Y 434
	Y	 T	CTT  L 389	L ATT	R CCA	GAA  E 398 ATC	V CTG	 I	CAC H. 407 ATC	P AAC	TTA L AAA	GCA A 416 GTC	TTG	S CCA	CAT  H 425	Ω	Q	TAT  Y 434
	TTT F	TAT	389 AAA  K	ATT	R CCA 	GAA  E 398 ATC  I 452	V CTG  L	I GTC	CAC H. 407 ATC I 461	P AAC	TTA L AAA K	GCA  A 416 GTC  V 470	TTG	CCA P	CAT H 425 ATG M 479	Q GTT 	Q TCC	TAT Y 434 ATC I 488
	TTT F	TAT	389 AAA  K	ATT	R CCA 	GAA  E 398 ATC  I 452	V CTG  L	I GTC  V	CAC H. 407 ATC I 461	CCT P AAC N GGT	TTA L AAA K	GCA  A 416 GTC  V 470 ATA	TTG L GCA	CCA P	CAT H 425 ATG M 479 ATT	GTT V	TCC  S	TAT Y 434 ATC I 488
	TTT F ACT	TAT Y CTC L	289 AAA K 443 TTG L	ATT I GCA A	R CCA P TTG	GAA E 398 ATC  I 452 GTT  V	V CTG L TAC TAC	GTC	CAC H 407 ATC I CCA P	AAC N GGT G	TTA L AAA K GTG V	GCA A 416 GTC V 470 ATA I	TTG L GCA A	S CCA P GCA A	CAT H 425 ATG M 479 ATT I 533	GTT V GTC	Q TCC  S CAA	TAT Y 434 ATC I 488 CTT L
	TTT F ACT	TAT Y CTC L AAT	389 AAA K 443 TTG L	ATT I GCA A ACC	R . CCA P TTG L	GAA  E 398 ATC  I 452 GTT  V	V CTG L TAC Y AAG	GTC V CTG	CAC H. 407 ATC 1 CCA P 515 TTT	AAC N GGT G CCA	AAA K GTG V CAT	GCA A 416 GTC V 470 ATA I 524 TGG	TTG L GCA A	S CCA P GCA A GAT	CAT H 425 ATG M 479 ATT I 533 AAG	GTC V	TCC S CAA Q ATG	TAT Y 434 ATC I 488 CTT L
	TTT F ACT T CAT	TAT Y CTC L AAT	389 AAA K 443 TTG L 497 GGA G 551	ATT I GCA A ACC	R . CCA P TTG L AAG	GAA  E 398 ATC  I 452 GTT  V 506 TAT  Y	V CTG L TAC Y AAG K	I GTC V CTG L AÁG	CAC H 407 ATC I CCA P 515 TTT F	AAC N GGT G CCA P	AAA  K GTG V CAT H	GCA A 416 GTC V 470 ATA I 524 TGG W 578 TTT	TTTG L GCA A TTTG L GCT	GCA A GAT D GTA	CAT H 425 ATG M 479 ATT I 533 AAG K 587 CTG	GTC V TGG W CAT	CAA Q ATG	TAT Y 434 ATC I 488 CTT L 542 TTA L
	TTT F . ACT T CAT H ACA	TAT Y CTC L AAT N AGA	389 AAA K 443 TTG L 497 GGA G 551	ATT I GCA A CC T CAG	R . CCA P TTG L AAG K . TTT	GAA E 398 ATC I 452 GTT V 506 TAT Y 560 GGG	V CTG L TAC Y AAG K CTT	I GTC V CTG  L AÁG	CAC H 407 ATC I CCA P 515 TTT F 569 AGT	AAC N GGT G TTC TTC	AAA K GTG V CAT H	GCA A 416 GTC V 470 ATA I 524 TGG W 578 TTT	TTG L GCA A TTG L GCT	GCA A GAT D GTA	CAT H 425 ATG M 479 ATT I 533 AAG K 587 CTG	GTC V TGG W CAT	CAA Q ATG	TAT Y 434 ATC I 488 CTT L 542 TTA L
	TTT F ACT T CAT H ACA T	TAT Y CTC L AAT N AGA R	389 AAA  K 443 TTG L 497 GGA G 551 AAG K 605	ATT I GCA A CC T CAG	R CCA P TTG L AAG K TTT F	GAA E 398 ATC I 452 GTT V 506 TAT Y 560 GGG G	V CTG L TAC Y AAG K CTT L ATG	I GTC V CTG L AÁG K	CAC H 407 ATC I CCA P 515 TTT F 569 AGT S	AAC N GGT CCA P TTC F	L AAA K GTG V CAT H	GCA A 416 GTC V 470 ATA I 524 TGG W 578 TTT F	TTTG L GCA A TTG L GCT A	S CCA P GCA A GAT D GTA V	CAT H 425 ATG M 479 ATT I 533 AAG K 587 CTG L	GTC V TGG W CAT	CAA Q ATG M GCA	TAT Y 434 ATC I 488 CTT L 542 TTA L 596 ATT I

GCA	TAT	659 CAA	CAG	GTC		CAA	AAT	677 AAA	GAA	GAT	686 GCC	TGG	ATT	695 GAG	CAT	GAT	704 GTT
A	Y	Q	Q	V	Q	Q	N	K	E	D	A	W	I	Ε	H	D	v
		713			722			731			740			749			758
TGG	AGA	ATG	GAG	ATT	TAT	GTG	TCT	CTG	GGA	ATT	GTG	GGA	TTG	GCA	ATA	CTG	GCT
W	R	М	E.	I	Y	V	S	L	<u> </u>	I	V	G	L	_A_	<u> I</u>	L.	_ <u>A</u>
		767			776			785			794			803			812
CTG	TTG		GTG	ACA		ATT	CCA		GTG	AGT		TCT	TTG		TGG	AGA	
		<b>-</b>															
<u>L</u>	L	A	<u>v</u>	T	S	I	P	\$	<u>v</u>	S	. D	S	L	T	W	R	E,
		821			830			839			848			857			866
TTT	CAC		ATT	CAG		AAG	CTA		ATT	GTT					GGC	ACA	
F	H	Y	Ι	Q	S	K	L	G	I	V	\$	L	L	L.	G	T	<u> </u>
		875			884			893			902			911		٠	920
CAC	GCA		ATT	TTT		TGG	AAT		TGG	ATA		ATA	AAA		TTT	GTA	
H	A	L	I	F	A	W	N	<u>K</u>	W	I	D	I	K	Q	F	V	W.
		929			938			947			956			965			974
TAT	ACA		CCA	ACT		ATG	ATA		GTT	TTC		CCA	ATT		GTC	CTG	
Y	T	P.	P	T	F	M	I	A	V	F	L	P	I	V.	V	L	<u> </u>
		983			992		1	1001		•	1010		1	019		,	L028
TTT	AAA		ATA	CTA		CTG			TTC				-				
									110	2002	AAG	AAG	ATA	CTG	AAG		
F											AAG	AAG	ATA	CTG	AAG		
	ĸ	s	I			L					AAG  K	AAG  K	 I	L	AAG  K		 R
			I	L	F	L.	 P			 R	 K		ī	L		ī	
CAT		1037		L	<b>F</b>		<b>P</b>	 С 1055	L L	 R	 K L064		 I	L 1073	к 		1082
CAT	:	1037		L	<b>F</b>	ACC	<b>P</b>	 С 1055	L L	 R	 K L064		 I	L 1073	к 		1082 TTG
CAT  H	:	1037		L	<b>F</b>		<b>P</b>	 С 1055	L L	 R	 K L064		 I	L 1073	к 		1082
	GGT  G	1037 TGG  W	GAA  E	GAC D	F 1046 GTC  V	ACC T	P AAA 	C 1055 ATT	L AAC	R AAA K	 K 1064 ACT  T	K GAG	I ATA I	L 1073 TGT	TCC	I CAG	U082 TTG
 Н	GGT - <del></del> G	1037 TGG  W	GAA  E	GAC D	F 1046 GTC  V	ACC  T	P AAA K	C 1055 ATT  I	AAC	R AAA K	 K 1064 ACT  T	K GAG  E	I ATA I	L 1073 TGT  C	TCC	CAG	1082 TTG  L
 Н	GGT  G	1037 TGG  W	GAA  E	GAC D	F 1046 GTC  V	ACC  T	P AAA K	C 1055 ATT  I	AAC	R AAA K	 K 1064 ACT  T	K GAG  E	I ATA I	L 1073 TGT  C	TCC	CAG	1082 TTG  L
 Н	GGT - <del></del> G	1037 TGG  W	GAA  E	GAC D	F 1046 GTC  V	ACC  T	P AAA K	C 1055 ATT  I	AAC	R AAA K	 K 1064 ACT  T	K GAG  E	I ATA I	L 1073 TGT  C	TCC	CAG	1082 TTG  L
H TAG	GGT G G AAT	LO37 TGG  W LO91 TAC 	GAA E TGT	GAC D TTA L	F LO46 GTC V L100 CAC H	ACC T ACA T	P AAA K TTT	C LOSS ATT I LOSS TTG	AAC N	R AAA K AAT N	K LO64 ACT T I118 ATT	GAG E GAT	ATA I ATA I ATA	L 1073 TGT  C 1127 TTT	TCC S TAT	CAG O CAC H	L L 1136 CAA
H TAG	GGT G G AAT N	L037 TGG W L091 TAC Y	GAA  E TGT  C	GAC D TTA L	V 100 CAC H	ACC T T ACA	AAA K	C 1055 ATT  I 1109 TTG  L	AAC N	R AAA K AAT N	K 1064 ACT T 1118 ATT  I	GAG E GAT D	ATA I ATA I ATA	L 1073 TGT C 1127 TTT F 1181	TCC S TAT	CAG O CAC H	1082 TTG L 1136 CAA  Q
H TAG	GGT G G AAT	L037 TGG W L091 TAC Y	GAA  E TGT  C	GAC D TTA L	V 100 CAC H	ACC T T ACA	AAA K	C 1055 ATT  I 1109 TTG  L	AAC N	R AAA K AAT N	K 1064 ACT T 1118 ATT  I	GAG E GAT D	ATA I ATA I ATA	L 1073 TGT C 1127 TTT F 1181	TCC S TAT	CAG O CAC H	1082 TTG L 1136 CAA  Q

K

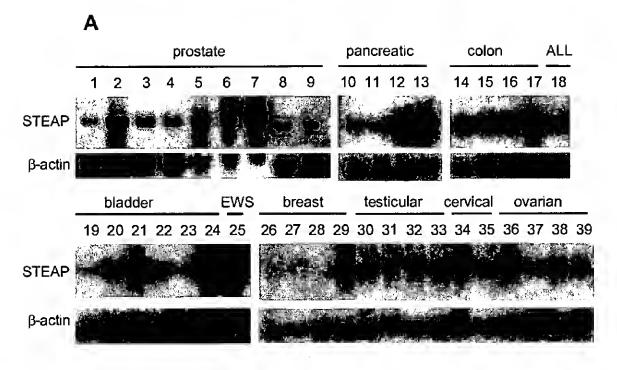
# FIG. 1C

## FIG. 4A

ATACTATTTTA TAGAATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGG AGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGC GTGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATT CACCCCTTAGCAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGG TTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAA GTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTT GCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCAT ATCAACAGGTCCAACAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCT **AGAGAATTTCACTATATTCAG**GTAAATAATATATAAAATAACCCTAAGAGGTAAATCTTCTTTTTGTGTTTATGAT ATAGAATATGTTGACTTTACCCCATAAAAAATAACAAATGTTTTTCAACAGCAAAGATCTTATACTTGTTCCAATT  $\tt CTCTGTTGCCCATGCTGGAGTACAGTGGCACGATCTCGGCTCACTGCAACCTGCGCCTCCTGGGTTCAGGCGATTC$ TCTTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACCCATCACCATGTCCAGCTAATTTTTGTATTTTTAGTA GAGACAGGGTTTTCCCATGTTGGCCAGGCTGGTCTCGATCTCCTGACCTCAAATGATCCGCCCACCTCGGCCTCCC AAAGTGCTGGGATGACAGTTGTGAGCCACCACACTCAGCCTGCTCTTTCTAATATTTGAAACTTGTTAGACAATTT TGTCACCTGAATTTAGTAATGCCTTTTATGTTACACAACTTAGCACTTTCCAGAAACAAAAACTCTCTCCTTGAAA TAATAGAGTTTTTATCTACCAAAGATATGCTAGTGTCTCATTTCAAAGGCTGCTTTTTCCAGCTTACATTTTATAT ACTTACTCACTTGAAGTTTCTAAATATTCTTGTAATTTTAAAACTATCTCAGATTTACTGAGGTTTATCTTCTGGT GGTAGATTATCCATAAGAAGAGTGATGTGCCAGAATCACTCTGGGATCCTTGTCTGACAAGATTCAAAGGACTAAA TTTAATTCAGTCATGAACACTGCCAATTACCGTTTATGGGTAGACATCTTTGGAAATTTCCACAAGGTCAGACATT CGCAACTATCCCTTCTACATGTCCACACGTATACTCCAACACTTTATTAGGCATCTGATTAGTTTGGAAAGTATGC CTCCATCTGAATTAGTCCAGTGTGGCTTAGAGTTGGTACAACATTCTCACAGAATTTCCTAATTTTGTAGGTTCAG CCTGATAACCACTGGAGTTCTTTGGTCCTCATTAAATAGCTTTCTTCACACATTGCTCTGCCTGTTACACATATGA TGAACACTGCTTTTTAGACTTCATTAGGAATTTAGGACTGCATCTTGACAACTGAGCCTATTCTACTATATGTACA

ATACCTAGCCCATAATAGGTATACAATACACATTTGGTAAAACTAATTTTCAACCAATGACATGTATTTTTCAACT A GTAACCTAGAAATGTTTCACTTAAAATCTGAGAACTGGTTACACTACAAGTTACCTTGGAGATTCATATATGAAAACGCAAACTTAGCTATTTGATTGTATTCACTGGGACTTAAGAATGCGCCTGAATAATTGTGAGTTCGATTTGTTCT GGCAGGCTAATGACCATTTCCAGTAAAGTGAATAGAGGTCAGAAGTCGTATAAAAGAGGTGTTGTCAGAACACCGT TGAGATTACATAGGTGAACAACTATTTTTAAGCAACTTTATTTGTGTAGTGACAAAGCATCCCAATGCAGGCTGAA ATGTTTCATCACATCTCTGGATCTCTCTATTTTGTGCAGACATTGAAAAAATTGTTCATATTATTTCCATGTTATC CATTAGTCGCCTTCACAACTGATAAAGATCACTGAAGTCAAATTGATTTTTGCTATAATCTTCAATCTACCTATAT TTCACTTAGACAGCTTGGAGACAAGAAATTACCCAAAAGTAAGGTGAGGAGGATAGGCAAAAAGAGCAGAAAGATG TGAATGGACATTGTTGAGAAATGTGATAGGAAAACAATCATAGATAAAGGATTTCCAAGCAACAGAGCATATCCAG ATGAGGTAGGATGGGATAAACTCTTATTGAACCAATCTTCACCAATTTTGTTTTTTCTTTTTGCAGAGCAAGCTAGGA CCTGCCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAG ATATGTTCCCAGTTGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTTATCACCAACATTTCA 

FIG. 5



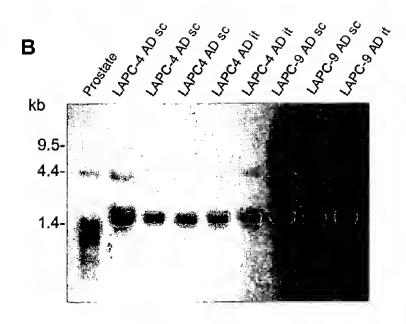
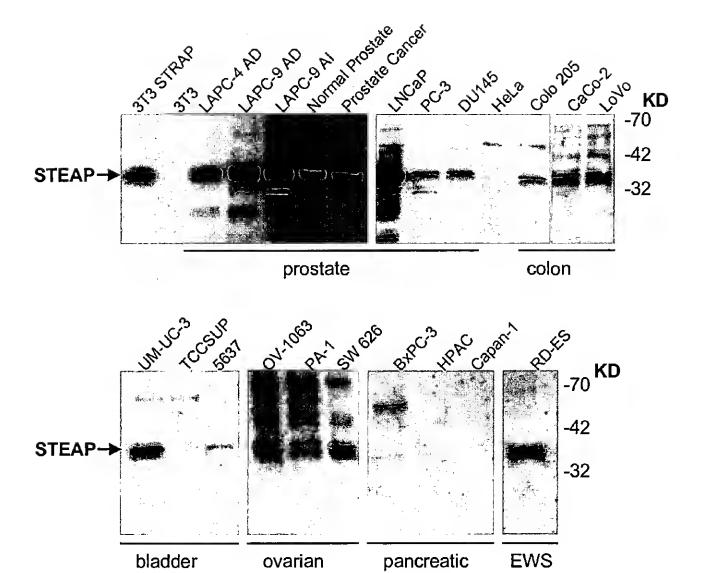
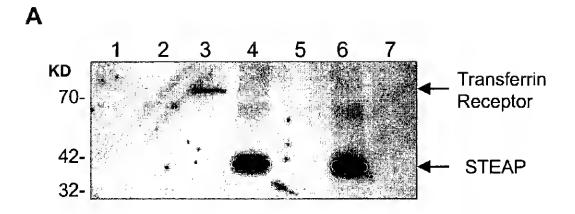
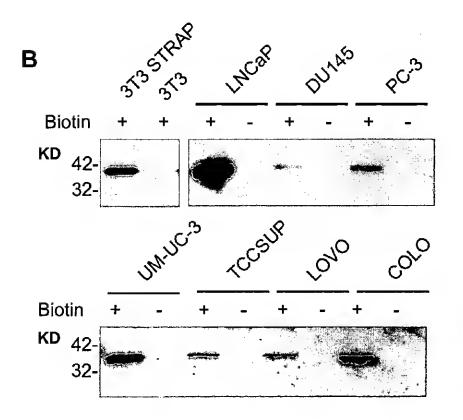


FIG. 6



**FIG.** 7





	(SEC	1 <b>(II</b> )	NO:5															
5 ' <sub>.</sub>	GGA	CGC	10 GTG	GGC	GGA	19 CGC	GTG	GGT	28 TCC	TCG	GGC	37 CCT	CGG	CGC	46 CAC	AAG	CTG	55 TCC
	GGG	CAC	64 GCA	GCC	сст	73 AGC		GCG			CCA	91 AGC	cee	CCT	100 CCG			109
			118			1:27			136			145			 154			 163
	CTC	CTT		TCT									TGG	GTA	GGC	GGG	GAA	GCA
	GCT	GGA	172 GTG	CGA	CCG	CCA	. CGG	CAG	CCA	CCC.	TGC	199 AAC	CGC	CAG	208 TCG	GAG	GTG	217 CAG
	TCC	GTA	226 GGC	ССТ		235 CCC						253 GGA	GTC	GGC	262 GCC	GCT		271
			280			 289			 298			307			<del></del> 316	<b></b> -		 325
	GAG	CTG	334	GGC	TCG									GGG 			GAG	
	ATT	CTT	GGT	GAT	CTT	GGA	AGT	GTC	CGT	ATC	ATG		TCA				ATG	379 GGA
							(SEC	) ID į	NO:6	)	➤ M	E	s	I	s	M	M	G
	AGC	CCT	388 AAG	AGC	CTT	397 AGT	GAA	ACT	406 TGT	TTA	CCT	415 AAT	GGC	ATA	424 AAT	GGT	ATC	433 AAA
	s	P	ĸ	s	L	s	E	T	С	L	P	N	<b>-</b>	I	N	G	ī	ĸ
	GAT	GCA	442 •AGG	AAG	GTC	451 ACT	GTA	GGT	460 GTG	ATT	GGA	469 AGT	GGA	GAT	478 TTT	GCC	AAA	487 TCC
	D	A	R	K	V	T						s						
	TTG	ACC	496 ATT	CGA	CTT	505 ATT	AGA	TGC	514 GGC	TAT	CAT	523 GTG	GTC	ATA	532 GGA	AGT	AGA	541 AAT
	L	T	I	R	L	I	R	С	G	Y	H	v	v	I	G	S	R	N
	CCT	AAG	550 TTT	GCT			ттт		568 CCT	CAT	GTG	577 GTA	GAT	GTC	586 ACT	CAT	CAT	595 GAA
	P	ĸ	F	A	s	E	F	F	P	Н	v	v	D	v	Т	H	Н	E
	GAT	GCT	604 CTC	ACA	AAA			ATA				631 GCT					CAT	
	D	A	L	T	ĸ	Т	N	I	I	F	v	A	I	H	R	E	H	Y
	ACC	TCC	658 CTG	TGG		667 CTG				CTT		685 GGT				ATT	GAT	703 GTG
	т	s	L	W		L		Н			v	 G	ĸ	ī		ī	D	
	ACC	<b>አ</b> አጠ	712	<b>አ</b> መረግ			830		730			739			748			757
	AGC	AAI	AAC	AIG		ATA		CAG		CCA	GAA	TCC					TTG	

ATOU CITYOUT FIGURE SHIPE FOR .

		766			775			784			793			802			811
TCA	TTA	TTC	CCA	GAT	TCT	TTG	ATT	GTC	AAA	GGA	TTT	AAT	GTT	GTC	TCA	GCT	TGG
s	L	F	P	D.	S	L	I	V	K	G	F,	N	v	v	s	A	W
		820															
GCA	CTT	CAG	TTA	GGA	CCT	AAG 	GAT	GCC	AGC	CGG	CAG	GTT	TAT	ATA	TGC	AGC	AAC
A	L	Q	L	G	P	K	D	A	S	R	Q	V	Y	I	С	S	N
		874			883									910			919
AAT	ATT	CAA	GCG 	CGA	CAA	CAG	GTT	ATT	GAA	CTT	GCC	CGC	CAG	TTG	AAT	TTC	ATT
N	I	Q	A <sub>.</sub>	R	Q	Q	V	I	E	L	A	R	Q	L	N	F	I
		928			937						955			964			973
					<b>-</b>									AAT			
P	I	D	L	G	S	L	s	S	A	R	E	I	E	N	L	P	<u>r</u>
	an a	982	T 65	<b>a</b> ma	991									1018			1027
														AGC			
R	L	F	T	L	W	R	G	. P	v	V	V	A	I	S	L	A	<u>T</u>
mmm		1036			1045									1072			1081
TTT			CTT	TAT	TCC		GTC	AGA	GAT	GTG	ATT	CAT	CCA	TAT	GCT	AGA	AAC
F	F	F	L	Y.	s	F	V	R	D	V	I	H	P	Y	A	R	N
-		1090			1099			1108			117			126		_	1135
									A.I.A								
					TAC												
						 К									T		 P
Q	Q	 S 1144	D	 F	Y 1153	к		P 1162	ī	E	I 171	<u>v</u>	N	K L180	 T	L.	<u>P</u>
Q	Q	 S 1144	D	 F	Y 1153	к		P 1162	ī	E	I 171	<u>v</u>	N	ĸ	 T	L.	<u>P</u>
Q .	Q GTT	S 1144 GCC	D ATT	F ACT	Y 1153 TTG	K CTC	TCC	P 1162 CTA	I GTA	E TAC	I 171 CTT	<u>v</u> GCA	N GGT	K L180	T CTG	L GCA	P 1189 GCT
Q ATA	Q GTT V	S 1144 GCC  A	D ATT	F ACT T	Y 1153 TTG  L	K CTC L	TCC  S	P 1162 CTA  L	I GTA  V	E TAC Y	I 171 CTT  L	V GCA 	N GGT  G	K 180 CTT  L	T CTG  L	GCA A	P 1189 GCT  A
Q ATA	Q GTT V	S 1144 GCC  A	D ATT	F ACT T	Y 1153 TTG  L	K CTC L	TCC  S	P 1162 CTA  L	I GTA  V	E TAC Y	I 171 CTT  L	V GCA 	N GGT  G	K 180 CTT  L	T CTG  L	GCA A	P 1189 GCT  A
Q ATA	Q GTT V	S 1144 GCC  A 1198 CAA	D ATT	F ACT T	Y 1153 TTG  L 1207 TAC	K CTC L GGC	TCC S	P 1162 CTA  L 1216 AAG	GTA V TAT	E TAC Y	I 171 CTT  L 225 AGA	GCA A	N GGT  G CCA	K 180 CTT  L	TGG	I GCA A	P 1189 GCT  A
Q ATA I	Q GTT V	S 1144 GCC A 1198 CAA CAA Q	ATT I CTT L	F ACT T TAT Y	1153 TTG  L 1207 TAC  Y	K CTC L GGC	TCC S ACC	P 1162 CTA  L 1216 AAG  K	GTA V TAT Y	TAC Y AGG R	I 171 CTT  L 225 AGA  R	GCA A TTT	GGT  G CCA	K 1180 CTT  L 234 CCT  P	TGG	I GCA A TTG	P GCT A 1243 GAA 
Q ATA I GCT A ACC	Q GTT V TAT Y	S 1144 GCC A 1198 CAA CAA CAA CAA CAA CAA CAA CAA CAA CA	D ATT	F ACT TAT Y TGT	1153 TTG  L 1207 TAC  Y	CTC L GGC G	TCC S ACC T CAG	P 1162 CTA  L 1216 AAG  K	GTA V TAT Y GGA	TAC Y AGG R TTA	I 171 CTT L 225 AGA R 279 CTA	GCA A TTT F	GGT G CCA P	180 CTT  L 234 CCT  P	TGG	I GCA A TTG	P GCT A 1243 GAA 
Q ATA I GCT A ACC	Q GTT V TAT Y	S 1144 GCC A 1198 CAA CAA CAA CAA CAA CAA CAA CAA CAA CA	D ATT	F ACT TAT Y TGT	1153 TTG  L 1207 TAC  Y	K CTC L GGC	TCC S ACC T CAG	P 1162 CTA  L 1216 AAG  K	GTA V TAT Y GGA	TAC Y AGG R TTA	I 171 CTT L 225 AGA R 279 CTA	GCA A TTT F	GGT G CCA P	L 180 CTT  L 234 CCT  P	TGG	GCA A TTG L GCT A	P GCT A 1243 GAA 
Q ATA I GCT A ACC	Q GTT V TAT Y	S 1144 GCC A 1198 CAA Q 1252 TTA L	D ATT I CTT L CAG	TAT Y TGT	1153 TTG  L 1207 TAC  Y 1261 AGA  R	CTC L GGC G AAA K	TCC S ACC T CAG	P 1162 CTA  L 1216 AAG  K	I GTA	TAC Y  AGG R  TTA L	I 171 CTT  L 225 AGA  R 279 CTA  L	GCA A TTT F AGT	GGT G CCA P TTT F	180 CTT  L 234 CCT  P	TGG W	GCA A TTG L GCT A	P 189 GCT A 1243 GAA  ATG 1351
Q ATA I GCT A ACC T GTC	Q GTT V TAT Y TGG W CAT	S 1144 GCC A 1198 CAA Q 1252 TTA L 1306 GTT	D ATT I CTT L CAG	TAT Y TGT C	1153 TTG  L 1207 TAC  Y 1261 AGA  R	GGC G AAA K CTC	TCC S ACC T CAG Q TGC	P 1162 CTA  L 1216 AAG  K 1270 CTT  L	TAT Y GGA G CCG	TAC Y  AGG R  TTA L  ATG	I 171 CTT  L 225 AGA  R 279 CTA  L	GCA A TTT F AGT S	GGT G CCA P TTT F	180 CTT  L 234 CCT  P 1288 TTC  F	TGG W	GCA A TTG L GCT A	P 189 GCT A 1243 GAA  ATG 1351
Q ATA I GCT A ACC T GTC	Q GTT V TAT Y TGG W CAT	S 1144 GCC A 1198 CAA Q 1252 TTA L 1306 GTT	D ATT I CTT L CAG	TAT Y TGT C	1153 TTG  L 1207 TAC  Y 1261 AGA  R	GGC G AAA K CTC	TCC S ACC T CAG Q TGC	P 1162 CTA  L 1216 AAG  K 1270 CTT  L	TAT Y GGA G CCG	TAC Y  AGG R  TTA L  ATG	I 171 CTT  L 225 AGA  R 279 CTA  L	GCA A TTT F AGT S	GGT G CCA P TTT F	180 CTT  L 234 CCT  P	TGG W	GCA A TTG L GCT A	P 189 GCT A 1243 GAA  ATG 1351 TTG
Q ATA I GCT A ACC T GTC V	Q GTT V TAT Y TGG W CAT H	S 1144 GCC A 1198 CAA Q 1252 TTA L 1306 GTT V	D ATT I CTT L CAG	TAT Y TGT C TAC	Y 1153 TTG  L 1207 TAC  Y 1261 AGA  R 1315 AGC  S	CTC GGC G AAA K CTC	TCC S ACC T CAG TGC CC	P 1162 CTA L 1216 AAG K 1270 CTT L 1324 TTA L	I GTA	TAC Y  AGG R  TTA L  ATG M	I 171 CTT  L 225 AGA  R 279 CTA  L .333 AGA  R	GCA A TTT F AGT S	GGT G CCA P TTT F TCA S	180 CTT  L 234 CCT  P 1288 TTC  F	TGG	GCA TTG A TAT Y	P 189 GCT A 1243 GAA  ATG 1351 TTG  L
Q ATA I GCT A ACC T TTT	Q GTT V TAT Y TGG W CAT H	S 1144 GCC A 1198 CAA Q 1252 TTA L 1306 GTT V	ATT I CTT L CAG Q GCC A ATG	TAT Y TGT TAC TAC TAC GCT	Y 1153 TTG L 1207 TAC Y 1261 AGA R 1315 AGC S	GGC G AAA K CTC L CAG	TCC S ACC T CAG Q CAG CCAG	P 1162 CTA L 1216 AAG K 1270 CTT L 1324 TTA L 1378 GTT	TAT Y GGA G CCG P	TAC Y  AGG R  TTA L  ATG M  GCA	I 171 CTT  L 225 AGA  R 279 CTA  L .333 AGA  R	GCA F AGT S AGG -R	GGT G CCA P TTT F TCA S GAA	180 CTT  L 234 CCT  P 1288 TTC  F	TGG	GCA A TTG A TAT Y TGG	P 189 GCT A 1243 GAA  ATG 1351 TTG  L 1405 AAT
Q ATA I GCT A ACC T TTT	Q GTT V TAT Y TGG W CAT H	S 1144 GCC A 1198 CAA Q 1252 TTA L 1306 GTT V	ATT I CTT L CAG Q GCC A ATG	TAT Y TGT TAC TAC TAC GCT	Y 1153 TTG L 1207 TAC Y 1261 AGA R 1315 AGC S	GGC G AAA K CTC L CAG	TCC S ACC T CAG Q CAG CCAG	P 1162 CTA L 1216 AAG K 1270 CTT L 1324 TTA L 1378 GTT	TAT Y GGA G CCG P	TAC Y  AGG R  TTA L  ATG M  GCA	I 171 CTT  L 225 AGA  R 279 CTA  L .333 AGA  R	GCA F AGT S AGG -R	GGT G CCA P TTT F TCA S GAA	180 CTT  L 234 CCT  P 1288 TTC  F	TGG	GCA A TTG A TAT Y TGG	P 189 GCT A 1243 GAA  ATG 1351 TTG  L 1405 AAT
Q ATA I GCT A ACC T TTT F	Q GTT V TAT Y TGG W CAT H	S 1144 GCC A 1198 CAA Q 1252 TTA L 1306 GTT V	D ATT I CTT L CAG Q GCC A ATG	TAT Y TGT C TAC Y TAC TAC	Y 1153 TTG L 1207 TAC Y 1261 AGA R 1315 AGC S 1369 TAT Y	GGC G AAA K CTC L CAG Q	TCC S ACC T CAG Q CAG CAG	P 1162 CTA L 1216 AAG K 1270 CTT L 1324 TTA L 1378 GTT V	TAT Y GGA G CCG P	TAC Y  AGG R  TTA L  ATG M  GCA A	I 171 CTT  L 225 AGA  R 279 CTA  L 333 AGA  R	GCA A TTT F AGT S AGG R ATT	GGT G CCA P TTT F TCA S GAA E	180 CTT  L 234 CCT  P 1288 TTC  F 342 GAG  N	TGG	GCA A TTG A TAT Y TGG W	P 189 GCT A 1243 GAA  ATG 1351 TTG  L 1405 AAT  N
Q ATA I GCT A ACC T TTT F GAG	Q GTT V TAT Y TGG W CAT H GAA	S 1144 GCC A 1198 CAA Q 1252 TTA L 1306 GTT V 1360 AAC N	D ATT I CTT L CAG Q GCC A ATG	TAT Y TGT TAC TAC TGG TGG	Y 1153 TTG L 1207 TAC Y 1261 AGA R 1315 AGC S 1369 TAT Y	GGC G AAA K CTC L CAG Q ATT	TCC S ACC T CAG Q CAG CAG GAA	P 1162 CTA L 1216 AAG K 1270 CTT L 1324 TTA L 1378 GTT V	TAT Y GGA P CAT H TAT	TAC Y  AGG R  TTA L  ATG A  ATC	I 171 CTT  L 225 AGA  R 279 CTA  L 333 AGA  N	GCA A TTT F AGT S ATT I TTT	GGT G CCA P TTT F GAA GAA E	180 CTT  L 234 CCT  P 288 TTC  F 342 GAG  E	TGG L TGG W TTC F AGA R TCT S	GCA TTG TTG TAT Y AGC	P 189 GCT A 1243 GAA E 1297 ATG 1351 TTG N 1405 AAT N

GGC	TTA	1468 CTT	TCC	UTC	1477 CTG	GCA	GTC	1486 ACT	TCT	ATC	1495 CCT	TCA	GlG	.504 AGC	AAT	GCT	1513 TTA
G	L	L	s	L	L	A	v	T	s	I	P	s	v	s	N	A	L
AAC		1522 AGA		TTC				1540 CAG						1558 GTC			1567 CTC
N	W	R	E	F	S	F	I	Q	S	Ŧ	L	G	Y	v	A	L	L
ATA 	AGT		TTC	CAT		TTA	ATT		GGA	TGG	AAA 	CGA	GCT	1612 TTT  F		GAA	GAG  E
		1630 AGA	ттт		1639 ACA			1648			1657			- 1666 GTT		1	L <b>6</b> 75
 Y	Y	R	F	Y	T	 P	P	n_n	 F	v	L	Α	L	 v	L_	 P	
	GTA		CTG	GAT	CTT	TTG	CAG		TGC	AGA	TAC	CCA	GAC	1720 TGA			729 ACT
GGA	_	L738 TGT												1774 GCC			.783 ATT
CCT	_	 1792 CTG	TCC		CAG	TTA	GGT	L810 GTA	CAT	GTG	ACT			1828 TGG	CCA	_	 .837 AGA
TGA		L846 CTC		1	1855		J	1864		:	1873			1882 CCT			891 TGC
TGC		900 GAT		GGA		AAC	AGG	AGC	CCT	GGC	1927 AGC	TGT	CTC	1936 CAG	AGG	ATC	.945 AAA
GCC	ACA			GAG			AGA		GAG	ACC		AAG		TTG		ACT	
CTA	CTT	2008 CCA 	CTG	CTT	TTC	CTG	CAT	TTA	AGC	CAT	TGT	AAA 	TCT	2044 GGG 	TGT	GTT	
	AGT	GAA	AAT	TAA	TTC	TTT 	CTG	ccc	TTC	AGT	TCT	TTA	TCC	TGA 	TAC	CAT	
ACA	CTG	TCT	GAA	TTA	ACT	AGA	CTG	CAA	TAA	TTC	TTT	CTT	TTG	AAA 2206	GCT	TT <b>T</b>	AAA 
			GCA	ATT	CAC	ATT	AAA 	ATT	ĠAT	TTT	CCA	TTG	TCA	ATT 	AGT	TAT	ACT
	TTT	CCT	GCC	TTG	ATC	TTT	CAT	TAG	ATA	TTT	TGT	ATC	TGC	TTG  2314	GAA	TAT	
	TTC	TTT	TTA	ACT	GTG	TAA	TTG	GTA	ATT	ACT	AAA 	ACT	CTG 	TAA  2368	TCT	CCA	AAA 
	TGC	TAT	CAA	ATT	ACA	CAC	CAT	GTT	TTC	TAT	CAT	TCT	CAT	AGA 	TCT	GCC 	TTA
	ACA	TTT	AAA 	TAA	AAA 	GTA	CTA	TTT	AAT	GAT	TTA	AAA	AAA	AAA 	AAA	AAA	AAA
	AAA	AAA	AAA	AAA	AAA			31									

## THUS UTTOOM ITO, TOWN SHIELD I OF S

Y V Y

## FIG. 10A-1

_						
	(SEQ ID NO:7	Dį .				
1			CCGGCCCGCG	GCGCGCACCG	TTGGCGCTGG	ACGCTTCCTC
					AACCGCGACC	
		(SEQ ID N	(O:8) → M E	K T C	I DAL	PLT
61	CTTGGAAGCG	CCTCTCCCTC	A <b>GTTATGG</b> AG	AAAACTTGTA	TAGATGCACT	TCCTCTTACT
	GAACCTTCGC	GGAGAGGGAG	TCAATACCTC	TTTTGAACAT	ATCTACGTGA	AGGAGAATGA
	•			•		
		S E K Q				F G R
121					GAACTGGTGA	
	TACTTAAGAA	GTCTTTTCGT	TCTCTGACAT	ACATAAAAAC	CTTGACCACT	AAAACCTTCT
						•
		LKML				R N P
181					TTTTTGGAAG	
	AGTGACCCTA	ACTTTTACGA	GGTCACACCA	ATAAGACAAC	AAAAACCTTC	AGCTTTGGGG
	0 W B		0 0 7	D 17 7		
0.4.2	-	T L L P				A A K
241					GCTATTCAGA	
	GTCTTCTGGT	GGGATGACGG	GTCACCACGT	CTTCAGAACT	CGATAAGTCT	TCGTCGGTTC
	K S G		ат и	י ע ק מ	Y D F L	T E L
301					ATGATTTTCT	
					TACTAAAAGA	
-	TTCAGACCGT	ATATTATA	ICGIIAGGIG	TOTOTOGTAA	TACTAAAAGA	GIGICITAAT
	TEV	LNGK	I L V	DISI	NNLK	I N O
361					ACAACCTCAA	
301					TGTTGGAGTT	
	1011010101			31311131331	10110011011	111101111011
	YPE	S N A E	YLA	HLVI	PGAH	V V K
421	TATCCAGAAT				CAGGAGCCCA	· ·
					GTCCTCGGGT	
	A F N	T I S A	WAL	Q S G A	A L D A	S R Q
481	GCATTTAACA	CCATCTCAGC	CTGGGCTCTC	CAGTCAGGAG	CACTGGATGC	AAGTCGGCAG
	CGTAAATTGT	GGTAGAGTCG	GACCCGAGAG	GTCAGTCCTC	GTGACCTACG	TTCAGCCGTC
	VFV	C G N D	S K A	K Q R V	M D-I	V R N
541	GTGTTTGTGT	GTGGAAATGA	CAGCAAAGCC	AAGCAAAGAG	TGATGGATAT	TGTTCGTAAT
	CACAAACACA	CACCTTTACT	${\tt GTCGTTTCGG}$	${\tt TTCGTTTCTC}$	ACTACCTATA	ACAAGCATTA
						·
					A K E I	
601					CCAAAGAAAT	
	GAACCTGAAT	GAGGTTACCT	AGTTCCTAGT	GAGTACCGTC	GGTTTCTTTA	ACTTTTCATC
						•
					S A V	
661					TGTCTGCTGT	
	GGGGACGTCG	ATAAAGGTTA	CACCTCCAAG	GGGAAGATAA	ACAGACGACA	CGACACACAG

F L F F Y C V I R D V I Y P

721 TTCTTGTTTT TCTATTGTGT TATAAGAGAC GTAATCTACC CTTATGTTTA TGAAAAGAAA AAGAACAAAA AGATAACACA ATATTCTCTG CATTAGATGG GAATACAAAT ACTTTTCTTT

D N T F K M A I S I P N R I F P I T A L 781 GATAATACAT TTCGTATGGC TATTTCCATT CCAAATCGTA TCTTTCCAAT AACAGCACTT CTATTATGTA AAGCATACCG ATAAAGGTAA GGTTTAGCAT AGAAAGGTTA TTGTCGTGAA T L L A L V Y L P G V I A A I L Q 841 ACACTGCTTG CTTTGGTTTA CCTCCCTGGT GTTATTGCTG CCATTCTACA ACTGTACCGA TGTGACGAAC GAAACCAAAT GGAGGGACCA CAATAACGAC GGTAAGATGT TGACATGGCT G T K Y R R F P D W L D H W M L C R K O 901 GGCACAAAAT ACCGTCGATT CCCAGACTGG CTTGACCACT GGATGCTTTG CCGAAAGCAG CCGTGTTTTA TGGCAGCTAA GGGTCTGACC GAACTGGTGA CCTACGAAAC GGCTTTCGTC LGLVALGFAFLHVL YTL VIP 961 CTTGGCTTGG TAGCTCTGGG ATTTGCCTTC CTTCATGTCC TCTACACACT TGTGATTCCT GAACCGAACC ATCGAGACCC TAAACGGAAG GAAGTACAGG AGATGTGTGA ACACTAAGGA IRYYVRW R ·L G NLTVTQA 1021 ATTCGATATT ATGTACGATG GAGATTGGGA AACTTAACCG TTACCCAGGC AATACTCAAG TAAGCTATAA TACATGCTAC CTCTAACCCT TTGAATTGGC AATGGGTCCG TTATGAGTTC KENPFST SSA WLSD SYV ALG 1081 AAGGAGAATC CATTTAGCAC CTCCTCAGCC TGGCTCAGTG ATTCATATGT GGCTTTGGGA TTCCTCTTAG GTAAATCGTG GAGGAGTCGG ACCGAGTCAC TAAGTATACA CCGAAACCCT I L G F F L F V L L G I T S L P S V S N 1141 ATACTTGGGT TTTTTCTGTT TGTACTCTTG GGAATCACTT CTTTGCCATC TGTTAGCAAT TATGAACCCA AAAAAGACAA ACATGAGAAC CCTTAGTGAA GAAACGGTAG ACAATCGTTA A V N W R E F R F V Q S K L G Y L T L I 1201 GCAGTCAACT GGAGAGAGTT CCGATTTGTC CAGTCCAAAC TGGGTTATTT GACCCTGATC CGTCAGTTGA CCTCTCTCAA GGCTAAACAG GTCAGGTTTG ACCCAATAAA CTGGGACTAG L C T A H T L V Y G G K R F L S P S N L 1261 TTGTGTACAG CCCACACCCT GGTGTACGGT GGGAAGAGAT TCCTCAGCCC TTCAAATCTC AACACATGTC GGGTGTGGGA CCACATGCCA CCCTTCTCTA AGGAGTCGGG AAGTTTAGAG R'WYL PAA Y V L G L I I P C T V L V 1321 AGATGGTATC TTCCTGCAGC CTACGTGTTA GGGCTTATCA TTCCTTGCAC TGTGCTGGTG TCTACCATAG AAGGACGTCG GATGCACAAT CCCGAATAGT AAGGAACGTG ACACGACCAC I K F V L I M P C V D N T L T R I 1381 ATCAAGTTTG TCCTAATCAT GCCATGTGTA GACAACACCC TTACAAGGAT CCGCCAGGGC TAGTTCAAAC AGGATTAGTA CGGTACACAT CTGTTGTGGG AATGTTCCTA GGCGGTCCCG W E R N S K H 1441 TGGGAAAGGA ACTCAAAACA CTAGAAAAAG CATTGAATGG AAAATCAATA TTTAAAACAA ACCCTTTCCT TGAGTTTTGT GATCTTTTTC GTAACTTACC TTTTAGTTAT AAATTTTGTT 1501 AGTTCAATTT AGCTGGATTT CTGAACTATG GTTTTGAATG TTTAAAGAAG AATGATGGGT TCAAGTTAAA TCGACCTAAA GACTTGATAC CAAAACTTAC AAATTTCTTC TTACTACCCA 1561 ACAGTTAGGA AAGTTTTTT CTTACACCGT GACTGAGGGA AACATTGCTT GTCTTTGAGA TGTCAATCCT TTCAAAAAAA GAATGTGGCA CTGACTCCCT TTGTAACGAA CAGAAACTCT 1621 AATTGACTGA CATACTGGAA GAGAACACCA TTTTATCTCA GGTTAGTGAA GAATCAGTGC TTAACTGACT GTATGACCTT CTCTTGTGGT AAAATAGAGT CCAATCACTT CTTAGTCACG

1681	AGGTCCCTGA	. C. STTATTT	CCCAGAGGCC	ATGGAGCTGA	G IGAGACT	AGCCTTGTG
	TCCAGGGACT	GAGAATAAAA	GGGTCTCCGG	TACCTCGACT	CTAACTCTGA	TCGGAACAC
	<b>ጥጥጥ</b> ሮ ልር ልር ጥ ል	<u>ስ ስር ስር ጥጥጥር</u> ር	ттсттатссс	CAACATCCAT	GACCTAATGT	CMMCCDARA
1,11					CTGGATTACA	
					• • • • • • • • • • • • • • • • • • • •	0.2.001111
1801					TGAGTTAAGT	
	GGTTATCTTC	ATAACGTCGA	AGGAAGAGAC	CGAGTTCCCG	ACTCAATTCA	CTTTCCTTTT
1061						
1861	ACAGCACAAT TCTCCTCTTA	CCACTGGTGA	GATAAAGGCT	TTATTAGGTA	TATCTGAGGA ATAGACTCCT	AGTGGGTCAC
	. I GICGIGIIA	CCACIGGIGA	CIAITICCGA	AATAATCCAT	ATAGACTCCT	TCACCCAGTG
1921	ATGAAATGTA	AAAAGGGAAT	GAGGTTTTTG	TTGTTTTTTG	GAAGTAAAGG	CAAACATAAA
					CTTCATTTCC	
1981					TGCTTTTCTT	
	ATAATGGTAC	TACTTAAGAT	CACTTTACTG	GGGAACTGAA	ACGAAAAGAA	TTATGTCTAT
2041		GGDACTATTT	ттатаасаса	እር <b>ል</b> አለአስጥጥጥ	ACAATTGATT	A
2011					TGTTAACTAA	
				1011111111111	TOT TANCETAL	TITICATAGG
2101	ATGTCTTGGA	TACATACGTA	TCTATAGAGC	TGGCATGTAA	TTCTTCCTCT	ATAAAGAATA
	TACAGAACCT	ATGTATGCAT	AGATATCTCG	ACCGTACATT	AAGAAGGAGA	TATTTCTTAT
						-
2161					TGGATTTCAC	
_	CCATATCCTT	TCTGACTTAT	TTTTACCTCC	CTATAGGGGA	ACCTAAAGTG	AACGTAACAC
2221	CAATAAGCAA	AGAAGGGTTG	ATAAAAGTTC	TTGATCAAAA	AGTTCAAAGA	AACCAGAATT
					TCAAGTTTCT	
	•					
2281					ATTAGGTTAA	
	AATCTGTCGT	TCGATTTATT	TATAACATTT	TAACGTGATA	TAATCCAATT	CATAATAAAT
2241	COMPONENT		3.3.3.Mmmma			<u></u>
2341					TGCTCAATAT ACGAGTTATA	
	CCATARIATI	AIACGAAACA	TITAMANIAI	AAGGIIIAIA	ACGAGITATA	AAAAG I AGA I
2401	TTAAATTAAT	TTCTAGTGTA	AATAAGTAGC	TTCTATATCT	GTCTTAGTCT	ATTATAATTG
					CAGAATCAGA	
2461	TAAGGAGTAA					
	ATTCCTCATT	TTAATTTACT	TATCAGACGT	CCATATTTAA	ACTTGTTACG	TATCTACTAG
2521	GAAAATTACG	CDADATCATA	GGGCAGAGAG	CTCTCAACAT	מראמיראמים אמי	CTCNNNTTTC
	CTTTTAATGC					
					nomorrana	Chelliana
2581	GATCTTTCTC	AAATCCTTGC	TGAAATTTAG	GATGGTTCTC	ACTGTTTTTC	TGTGCTGATA
	CTAGAAAGAG	TTTAGGAACG	ACTTTAAATC	CTACCAAGAG	TGACAAAAAG	ACACGACTAT
2641	GTACCCTTTC					
	CATGGGAAAG	GTTCCACTGG	AAGTUCCCCT	AATTGGAAGG	ATCGAGTTCG	TTACTCGATT
2701	AAGGAGCCTT	ATGCATGATC	<b>ፐፐ</b> ርርርልርልጥል	тсадалтаас	ТАВАВСССВС	<b>ТСВСТТТССС</b>
_,					ATTTTCCGTG	
		<b>-</b>				
2761	ATTTTTCTGC	CTGCTCTGCT	AAGACCTTTT	TTTTTTTTT	ACTTTCATTA	TAACATATTA
	TAAAAAGACG	GACGAGACGA	TTCTGGAAAA	AAAAAAAAA	TGAAAGTAAT	ATTGTATAAT

2821	TACATGACAT ATGTACTGTA	I. ACAAAAA ATATGTTTTT	TGATTAAAAT ACTAATTTTA	ATATTAAAAC TATAATTTTG	A. ATCAACA TTGTAGTTGT	ATCCAGGATA TAGGTCCTAT
2881		AAACTTTTTA TTTGAAAAAT				
2941		GTTTTTCTAA CAAAAAGATT				
3001		AGTCTTGCTC TCAGAACGAG				
3061		CTCCTCCCAG GAGGAGGGTC				
3121		ATGTGCCACT TACACGGTGA				
3181		GGTCAGGCTG CCAGTCCGAC				
3241		ATATTTTCTT TATAAAAGAA				
3301		TATTAAACAT ATAATTTGTA				
3361		TTTGCACTGA AAACGTGACT				
3421		GGATGAGGGT CCTACTCCCA				
3481		TTATTTATAA AATAAATATT				
3541		AACCCAAGCA TTGGGTTCGT				
3601		GACCCTACAG CTGGGATGTC				
3661		AACAGTTAGG TTGTCAATCC				
3721		TTTAGGTACC AAATCCATGG				
		AAAGAAGAGA TTTCTTCTCT				
3841		ATCCATAGGT TAGGTATCCA				
3901		AAATGCTCTA TTTACGAGAT				

3961	GAGCACTCTG	A. STTTTGG	CATAATAGCT	GCATTTCCAG	AL . IGACCTT	TGGCCCCAAC
	CTCGTGAGAC	TACCAAAACC	GTATTATCGA	CGTAAAGGTC	TGGACTGGAA	ACCGGGGTTG
4021	CACAAGTGCT	CCAAGCCCCA	CCAGCTGACC	AAAGAAAGCC	CAAGTTCTCC	TTCTGTCCTT
					GTTCAAGAGG	
4081					ACCATATTAA	
	GGGTGTTGGA	GGGACGAGGG	TTTTGATACT	TTAATTAAAC	TGGTATAATT	GTGTCGACTG
4141					AGATGAAAAT	
	AGGAGGTCAA	ATGAATTCCA	TCTTTCTTAC	TCAAATGTTG	TCTACTTTTA	TTCACGAAAC
4201					ATTTAAAAAA	
	CCGCTTGACA	TAAGGAAAAT	TGTCTAGGTT	TGATAAAATG	TAAATTTTT	TTTCAATTTG
4261	TAAACTTCTT	TACTGCTGAT	ATGTTTCCTG	TATTCTAGAA	AAATTTTTAC	ACTTTCACAT
	ATTTGAAGAA	ATGACGACTA	TACAAAGGAC	ATAAGATCTT	TTTAAAAATG	TGAAAGTGTA
4321	TATTTTTGTA	CACTTTCCCC	ATGTTAAGGG	ATGATGGCTT	TTATAAATGT	GTATTCATTA
					AATATTTACA	
1381	AATGTTACTT	TAAAAATAAA	AAAAAAAAA	АААААААА	AAAAAAA	
	TTACAATGAA	ATTTTTTTT	TTTTTTTTT	${\tt TTTTTTTTT}$	TTTTTTTT	

FIG. 10A-5

## FIG. 10B

## STEAP-2, AA508880 (NCI\_CGAP Pr6)

## STEAP-2, 98P4B6 SSH fragment

TTTGCAGCTTTGCAGATACCCAGACTGAGCTGGAACTGGAÁTTTGTCTTCCTATTGACTCTACTTCTTTAAAAGCG GCTGCCCATTACATTCCTCAGCTGTCCTTGCAGTTAGGTGTACATGTGACTGAGTGTTGGCCAGTGAGATGAAGTC TCCTCAAAGGAAGGCAGCATGTGTCCTTTTT (SEQ ID NO:10)

## STEAP-3, AI139607 (testis EST)

(SEQ 1D NO:11)

## STEAP 4, R80991 (placental EST)

ggccgcggcanccgctacgacctggtcaacctggcagtcaagcaggtcttggccanacaagagccacctctgggtg aaggaggagtctggcggatggagatctacctctccctgggagtgctggccctcggcacgttgtccctgctggccg tgacctcactgccgtccattgcaaactcgctcaactggaggagttcagcttcgttcagtcctcactgggctttgt ggccntcgtgctgagcacactncacacgctcacctacggctggacccgcgccttcgaggagagccgctacaagttctacctncctccaaccttcacgntcacgctggtgccctgcgttcgttcatcctgggccaaagccctgtttntactgccttgcattcagccgnaga \* (SEQ 1D NO:12)

# FIG. 11A-1

87 75 0	177 165 36 0	266 254 125 0	356 344 215 31
76 VVDVTHHEDALIKTN GAEVISYSEHAKKSG	166 ROVIIGSINIOARGO ROVEVEGNOSKAROR EDDELHEDTGETS	256 HENVIKTUENVALTI ESHPRIFFETTI HLVIKTEPAVSETTI HLVIKTEPAVSETTI	346 HANIENSWNEERVNE ILKKENPFSTSSAWL CONKEDANIEHDYNE WPXKSHLWVKEEVNE
61 IGSRNEKFASEFFPH FGSRNFOKTT-LLPS	16S VVSANALGLGPKDAS TISANALGSBALDAS QEELMKMK-PRRNLE	241 EPTARNOGSDEVKIH YETVYEKKONTERMA HELATSHOOYKVKIH	331 RSERYLFINMAXOOV YYVRWRICHLTVTOA RSYRYHIMMAYOOV AAXATTWSTWOSSRS
KBTTIRLIRGGYHYYY REHGLKMLOGGYSKY	136 LASLEPOSLIVKGFN LAHLVEGAHVNEAFNMESRKDITN	226 240 HATEFETSFVEDY ICVELFFCVIKDY IASLITEFTLEEVI	316 FANUTOAYSIICLPHR FAPTHULYTHUTH FAVITALETHUTHTH FAVITALETHUTHTH FAVITALETHUTHTH
ARKVIIVGVIBSIDDIA -KQEIVCIFGTIDIA	NIMRENOYPESINAEN NILKENOYPESINAEN NILKENOYPESINAEN	211 RIGHTLWRGEVVVXIS OLIEPWWRFFYLSAV BLEPONHLHIKIRNI	301 TWLOCREGIGIDSER HWRICERCHGIVALG KWMITERCEGIDSER
16 TGTENGINGIKD TGIDALHLTMNSSE-	106 DERHLEVERTITE EUTEVENSKEINE	196 LGSISSARETENLET OGSIMANKETEKYET ADEFDCPSELQH-TQ	300 LYYGTKYRRFPPWIE LYRGTKYRRFPDWIE HHNGTKYKKFPHWIE
1 MESISMMGSPKSLSE MEK	105 ETFVATHRENTSIN ETILATHRENTOFIT	181 VIELAROLINF-IRID WMDIVRNIGH-TEMB MLKRPVLHHIHOTAH	271 ISLVXTAGLLANAYG LALVXTEGYYANTLO LALVXTEGYTANIVU
2 STEAP2 3 STEAP3 4 STEAP1 5 STEAP4	2 STEAP2 3 STEAP3 4 STEAP1 5 STEAP4	2 STEAP2 3 STEAP3 4 STEAP1 5 STEAP4	2 STBAP2 3 STEAP3 4 STEAP1 5 STEAP4

# FIG. 11A-2

420 421 435 436 450 REHVLIYGWK RAFREYKRYTPPN KVIGHIUF-SIVHLD RAHTHVYGGK RFLSPENLKWYIPRA YVIGHIIRGTVIJIK MIHALIFAWN KWIDIKQFVWYTPPH FMIAVFHIIVVIHFK MIHALIFAWN KAFREBRYKRYTPPH FMIAVFHIIVVIHFK	
AXVE	
NWREFSFLOGTEGYV NWREPREVOSKIGYL TWREPHYLDSKLGIV NWREFSFVOGSLIGFV	481 454 459 CSQL 339
NAN	480 4
376 BLLAVTHIPSVSK VLIGITSLPSVSK ALIKATSIPSVSK SLIAVTHIPSIAK	66 OGWENSKH HGWEDVTKINK
SER ERES	465  ELXE
361 375 2 STEAP2 IEMYIBFGIMSLGIR 3 STEAP3 SDSYVALGINGFFIR 4 STEAP1 KETNYSLGINGTATI 5 STEAP4 KETNYSLGINGTATI 5 STEAP4	451 465 4 2 STEAP2 LLQÜCRYED 3 STEAP3 FVÜIMPGVDNTLTRÜ R 4 STEAP1 SIÜFLEGLRKKILKÜ R 5 STEAP4 AKAÜFXLÜCIOPX
TEAP2 TEAP3 TEAP1 TEAP4	ibap2 ibap3 ibap1 ibap4
បែម4 ៧ ស្រួលស្ល	១៩ ♣ ក ខ្លួល ខ្លួ

# FIG. 11B

STRAP-1	67	LFP(	WH.	LPI	KI	WI	IA	SLI	FL	YT]	<b>L</b> R	EV]	CHP	LA'	TSI	IOC	YF	YK.	[P]	LV	IN	KV	LI	'MV	SI	TLI
STRAP-2	208	LFT	WR	GPV	VV2	AIS	LA:	TFE	ΕL	YSE	VR	DV]	CHP	YAI	RNÇ	2QS	DF	YK.	[P]	ΕI	VN	KI	'LE	VI	AI	TLL
		**	*	*	4		*		**				***			*		* * 1			*	*	**	*		***
STRAP-1	127	ALV	LP	GVI	AA)	٤٧٥	LHI	NGT	'KY	KKI	PH	WL	)KW	ML:	ľRF	OF	'GL	LSI	FE	'AV	LH	ΑI	'YS	LS	YPI	MRR
STRAP-2	268	SLV	ZLA	GLI	AA7	١٧Q	LY'	YGT	KY	RRI	PP	WLE	CTW.	LQ	CRF	OL	GL	LSI	FE	'AM	VH	V.A	YS	LC	LPI	MRR
		***	*	*	**	*	*	**	**		* *		*					* * *			*		**	*		* * *
STRAP-1	187	SYRY	KL!	LNW	AY(	QV	QQi	NKE	DAI	WIE	HD	VWF	ME:	ΙΫ́	VSI	GI	VG.	LAJ	L	LL	ΑV	TS	IP	sv	SD:	SLT
STRAP-2	328																									
		* **			***			* *		* *			*		*			*						* *		*
STRAP-1	247	WREE	HY:	IOS	KLG	iv	SLI	LLG	TI	HAI	IF	AWN	IKW:	ID:	IKO	FV	wy	rpr	T F	мт	ΆV	ът.	PT	w	T.T	
STRAP-2	388	WREE	SF:	IQS	TLO	ΥV	ALI	LIS	TF	HVI	ΙY	GWI	(RA)	FEI	EEY	YR	FY:	rpi	NE	VL	AL	VL	PS	IV	ΤL	
_		****			**																					

# FIG. 11C

STEAP1	66	ELFPQWHLPIKIAAIIASLTFLYTLLREVIHPLATSHQQYFYKIPILVINKVLPMVSITL
STEAP3	195	QLFPMWRFPFYLSAVLCVFLFFYCVIRDVIYPYVYEKKDNTFRMAISIPNRIFPITALTL
STEAP1	126	LALVYLPGVIAAIVQLHNGTKYKKFPHWLDKWMLTRKQFGLLSFFFAVLHAIYSLSYPMR
STEAP3	255	LALVYLPGVIAAILQLYRGTKYRRFPDWLDHWMLCRKQLGLVALGFAFLHVLYTLVIPIR
STEAPi	186	RSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEIYVSLGIVGLAILALLAVTSIPSVSDSL
STEAP3	315	YYVRWRLGNLTVTQAILKKENPFSTSSAWLSDSYVALGILGFFLFVLLGITSLPSVSNAV  * * * * * * * * * * * * * * * * * * *
STEAP1	246	. $ \label{twrefhylosklgivslllgtihal} \textbf{TWREFHYIQSKLGIVSLLLGTIHALIFAWNKWIDIKQFVWYTPPTFMIAVFLPIVVLIFK} $
STEAP3	375	NWREFRFVQSKLGYLTLILCTAHTLVYGGKRFLSPSNLRWYLPAAYVLGLIIPCTVLVIK **** ***** * * * * * * * * * * * * * *
STEAP1	306	SILFLPCLRKKILKIRHGWEDVTK
STEAP3	435	FVLIMPCVDNTLTRIRQGWERNSK

# FIG. 11D

STEAP2	29	RKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGSRNPKFASEFFPHVVDVTHHEDALTKTNI
STEAP3	18	KQETVCIFGTGDFGRSLGLKMLQCGYSVVFGSRNPQ-KTTLLPSGAEVLSYSEAAKKSGI ** * ** * * * * * * * * * * * * * * *
STEAP2	89	IFVAIHREHYTSLWDLRHLLVGKILIDVSNNMRINQYPESNAEYLASLFPDSLIVKGFNV
STEAP3	77	IIIAIHREHYDFLTELTEVLNGKILVDISNNLKINQYPESNAEYLAHLVPGAHVVKAFNT * ****** * * * **** * ********** * * * *
STEAP2	149	VSAWALQLGPKDASRQVYICSNNIQARQQVIELARQLNFIPIDLGSLSSAREIENLPLRL
STEAP3	137	ISAWALQSGALDASRQVFVCGNDSKAKQRVMDIVRNLGLTPMDQGSLMAAKEIEKYPLQL ***** * ***** * * * * * * * * * * * *
STEAP2	209	FTLWRGPVVVAISLATFFFLYSFVRDVIHPYARNQQSDFYKIPIEIVNKTLPIVAITLLS
STEAP3	197	FPMWRFPFYLSAVLCVFLFFYCVIRDVIYPYVYEKKDNTFRMAISIPNRIFPITALTLLA * ** *
STEAP2	269	LVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQCRKQLGLLSFFFAMVHVAYSLCLPMRRS
STEAP3	257	LVYLPGVIAAILQLYRGTKYRRFPDWLDHWMLCRKQLGLVALGFAFLHVLYTLVIPIRYY **** * ** *** *** ** * * * ****** * * *
STEAP2	329	ERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALNW
STEAP3	317	VRWRLGNLTVTQAILKKENPFSTSSAWLSDSYVALGILGFFLFVLLGITSLPSVSNAVNW * * * * * * * * * * * * * * * * * * *
STEAP2	389	REFSFIQSTLGYVALLISTFHVLIYGWKRAFEEEYYRFYTPPNFVLALVLPSIVIL
STEAP3	377	REFRFVQSKLGYLTLILCTAHTLVYGGKRFLSPSNLRWYLPAAYVLGLIIPCTVLV

# FIG. 1A-1

	(SE	QI	M <del>G</del>	0:1)														
5'		•	11	•	CAA	20 GCT	AAG	GCG	AAG	AGT	GGG	TGG	CTG	AAG	CCA	TAC	TAT	TTT
			TTA				AGA			ATC				GAA	10 GAA		TGG	
(8	EQ.I	<b>10</b> -140	1:2)	<del>/&gt;</del> M	E	S	R	K	D	I	T	N	Q	E	E	L	W	K
	ATG	AAG	119 CCT		AGA		TTA	GAA		GAC			TTG		155 AAG	GAC	ACG	164 GGA
	M	K	P	R	R	N	L	E	E	D	D	Y	L	Н	K.	D	T	G
	GAG	ACC	173 AGC	ATG	CTA			CCT					TTG			ACA		218 CAT
	E	T	S	М	L	K	R	P	v	L	L	Н	L	Н	Q	T	A	Н
	_GCT	GAT	227 GAA	TTT	GAC		CCT	TCA		CTT			ACA			CTC		272 CCA
	A	D	E	F	D	С	P	s	E	L	Q	Н	T	Q	E	L	F	P
	CAG	TGG	281 CAC	TTG	CCA	290 ATT	AAA	ATA		GCT	ATT	308 ATA		TCT	317 CTG		TTT	326 CTT
	Q	W	Ħ	L_	P	I	K	I	A	A	I	I	A	s	L	T	F	L
	TAC	ACT	335 CTT	CTG	AGG			ATT		CCT		362 GCA	ACT	TCC		CAA		
	TAC		CTT			GAA	GTA		CAC	CCT	TTA	GCA	ACT	TCC	CAT.	CAA	CAA	TAT
	Y	T	CTT L 389	L	R	GAA  E 398	GTA  V	ATT	CAC H 407	CCT  P	TTA  L AAA	GCA  A 416	ACT T T	TCC  S	CAT. H 425 ATG	CAA Q GTT	CAA Q TCC	TAT Y 434 ATC
	Y	TAT	CTT L 389	L	R	GAA E 398 ATC	GTA V CTG	ATT  I	CAC H 407 ATC	CCT P P	TTA L AAA	GCA A A 416 GTC	ACT T T	TCC  S CCA	CAT. H 425 ATG	CAA Q GTT	CAA Q TCC	TAT  Y 434 ATC
	TTT	TAT Y	389 AAA K	L ATT	R CCA P	GAA  E 398 ATC  I 452	GTA V CTG L TAC	ATT I GTC V CTG	CAC  H 407 ATC  I 461 CCA	P AAC N GGT	TTA L AAA K GTG	GCA A 416 GTC V 470 ATA	ACT T TTG L GCA	TCC S CCA P	CAT. H 425 ATG M 479 ATT	CAA Q GTT V GTC	CAA Q TCC S CAA	TAT Y 434 ATC I 488 CTT
	TTT F ACT	TAT Y CTC	L 389 AAA K 443 TTG	L ATT	R CCA P	GAA E 398 ATC I 452 GTT	GTA V  CTG L  TAC	ATT I GTC V	CAC H 407 ATC I 461 CCA	AAC N	TTA L AAA K GTG	GCA  A 416 GTC  V 470 ATA	ACT T TTG L GCA	TCC S CCA P GCA	CAT. H 425 ATG M 479 ATT	CAA Q GTT V GTC	CAA Q TCC S CAA	TAT Y 434 ATC I 488 CTT
	TTTTF	TAT Y CTC	CTT L 389 AAA K 443 TTG L 497	ATT I GCA	R CCA P TTG	GAA E 398 ATC I 452 GTT V 506	GTA V CTG L TAC TAC	ATT I GTC V CTG	CAC H 407 ATC  I CCA  P	AAC N GGT	TTA L AAA K GTG V	GCA A 416 GTC V 470 ATA I	TTG L GCA	TCC S CCA P GCA A	CAT. H 425 ATG M 479 ATT I	CAA Q GTT V GTC V	CAA Q TCC S CAA Q	TAT Y 434 ATC I 488 CTT L
	TTTTF	TAT Y CTC L AAT	CTT L 389 AAA K 443 TTG L 497	ATT I GCA A ACC	R CCA P TTG L AAG	GAA E 398 ATC I 452 GTT V 506 TAT	CTG L TAC Y AAG	ATT I GTC V CTG	CAC H 407 ATC I CCA P 515 TTT	AAC N GGT G CCA	AAA  K  GTG  V  CAT	GCA A 416 GTC V 470 ATA I 524 TGG	TTG GCA TTG	TCC S CCA P GCA A GAT	CAT. H 425 ATG M 479 ATT I 533 AAG	GTT V TGG	CAA  TCC S  CAA  Q  ATG	TAT Y 434 ATC I 488 CTT L
	TTTT-F ACT-H ACA	TAT Y CTC L AAT N	X 389 AAA K 443 TTG L 497 GGA G 551 AAG	ATT I GCA A ACC T CAG	R CCA P TTG L AAG K TTT	GAA E 398 ATC I 452 GTT V 506 TAT Y	CTG L TAC Y AAG K CTT	ATT I GTC V CTG L AAG K	CAC H 407 ATC I CCA P 515 TTT F 569 AGT	AAC N GGT G CCA P	AAA K GTG V CAT H	GCA  A 416 GTC  V 470 ATA  I 524 TGG  W	TTG L GCA TTG GCA GCA GCT	CCA P GCA A GAT D	CAT- H 425 ATG M 479 ATT I 533 AAG K 587 CTG	GTC V TGG W CAT	CAA Q TCC S CAA Q ATG	TAT Y 434 ATC I 488 CTT L 542 TTA L
	TTTT-F ACT-H ACA	TAT Y CTC L AAT N	X 389 AAA K 443 TTG GGA G 551 AAG	ATT I GCA A ACC T CAG	R CCA P TTG L AAG K TTT	GAA E 398 ATC I 452 GTT V 506 TAT Y 560 GGG	CTG L TAC Y AAG K CTT	ATT I GTC V CTG L AAG K CTC	CAC H 407 ATC I CCA P 515 TTT F 569 AGT	AAC N GGT G CCA P	AAA K GTG V CAT H	GCA  A 416 GTC  V 470 ATA  I 524 TGG  W	TTG L GCA A TTG GCA A	GCA A GAT D GTA	H 425 ATG —— M 479 ATT —— I 533 AAG —— K 587 CTG	GTC V TGG W CAT	CAA Q TCC S CAA Q ATG M GCA	TAT Y 434 ATC I 488 CTT L 542 TTA L 596 ATT
	TTTT-F ACT-H ACA-T	TAT Y CTC L AAT N AGA	X 389 AAA K 443 TTG GGA G S 551 AAG K 605	ATT I GCA A ACC T CAG	R CCA P TTG L AAG K TTT F	GAA E 398 ATC I 452 GTT V 506 TAT Y 560 GGG G	CTG L TAC Y AAG K CTT L ATG	ATT I GTC V CTG L AAG K CTC	CAC H 407 ATC I CCA P 515 TTT F 569 AGT S 623	AAC N GGT G TTC F	AAA K GTG V CAT H TTT	GCA A 416 GTC V 470 ATA I 524 TGG W 578 TTT F	TTG L GCA A TTG GCA A	GCA A GAT D GTA V	ATT H 425 ATG M 479 ATT I 533 AAG K 587 CTG L	CAA Q GTT V GTC V TGG W CAT	CAA Q TCC S CAA Q ATG M GCA A	TAT Y 434 ATC I 488 CTT L 542 TTA L 596 ATT I

# FIG. 1A-2

GCA  A	TAT	659 CAA 	CAG	GTC		CAA  O	AAT  N	677 AAA  K		GAT	686 GCC 	TGG  W	ATT  I	695 GAG  E	CAT  H	GAT	704 GTT
TGG	AGA	713	-	ATT	722			731			740			749 GCA			758 GCT
W	R.	М	Ε	I	Y_	V	s	L	G	I	V	G	L	Α.	I	L	A
CTG	TTG	767 GCT	GTG	ACA	776 TCT	ATT	CCA	785 TCT	GTG	AGT	794 GAC	TCT	TTG	803 ACA	TGG	AGA	812 GAA
<u>L</u>	L	A	v	T	S	I	P	S	<u>_v</u>	S	D	s	L	T	W	R	Ε.
T <b>TT</b>	CAC	821 TAT	ATT	CAG	830 AGC	AAG	СТА 	839 GGA	ATT	GTT	848 TCC	CTT	CTA	857 CTG	GGC	ACA	866 ATA
F	H	Y	I	Q	S	K	L	G	I	V	S	L	L	L	G	T	I
CAC	GCA	875 TTG	ATT	TTT	884 GCC	TGG	AAT	893 AAG	TGG	ATA	902 GAT	ATA	AAA	911 CAA	TTT	GTA	920 TGG
H	A	L	I	F	A	W	N	K	W	I	D	I	K	Q	F	V	W·
TAT  Y	ACA  T	929 CCT 	CCA  P		938 TTT 	ATG  M		947 GCT 			956 CTT  L	CCA 		965 GTT  <b>V</b>	GTC  V	CTG  L	974 ATA 
TTT	AAA	983 AGC	ATA	СТА	992 TTC	CTG		1001 TGC	TTG		1010 AAG	AAG		CTG	AAG		LO28 AGA
										 R		 К	 I	 L	 К	- <del>-</del> -	 R
<u> </u>	K	S	<u> </u>	٠	F			С		ĸ	K	K		ь	K	1	r
CAT		1037 TGG	GAA		1046 GTC				AAC		1064 ACT	GAG	-	1073 TGT	TCC		1082 T <b>T</b> G
Н	G	W	E	D	V	T	K	I	N	ĸ	T	E	I	С	s	Q	Γ
TAG 	AAT		TGT  C	TTA		ACA				AAT 				1127 TTT  F	TAT	CAC	L136 CAA  Q
CAT		1145 AAG	<b>TT</b> T		1154 TTT	GTT		1163 AAA 	ATG		1172 ATT	CAA		1181 AAA 	AAA 		1190 AAA 
H	F	K	F	V	F	V	N	K	М	I	I	Q	G	K	K	K	K

AAA AA 3' --- --K

# FIG. 1C

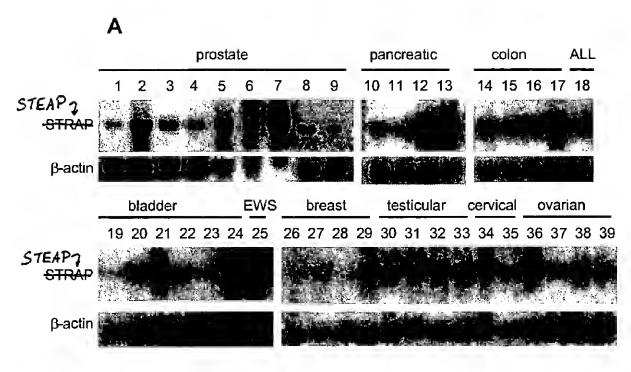
## FIG. 4A

ATACTATTTTATAGAATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGG AGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGC GTGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATT CACCCCTTAGCAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGC  $\tt TTTCCATCACTCTTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAA$ GTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTT GCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCAT ATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTTGGAGAATGGAGATTTATGTGTCTCT **AGAGAATTTCACTATATTCAG**GTAAATAATATATAAAATAACCCTAAGAGGTAAATCTTCTTTTTGTGTTTATGAT ATAGAATATGTTGACTTTACCCCATAAAAAATAACAAATGTTTTTCAACAGCAAAGATCTTATACTTGTTCCAATT CTCTGTTGCCCATGCTGGAGTACAGTGGCACGATCTCGGCTCACTGCAACCTGCGCCTCCTGGGTTCAGGCGATTC GAGACAGGGTTTTCCCATGTTGGCCAGGCTGGTCTCGATCTCCTGACCTCAAATGATCCGCCCACCTCGGCCTCCC AAAGTGCTGGGATGACAGTTGTGAGCCACCACACTCAGCCTGCTCTTTCTAATATTTGAAACTTGTTAGACAATTT TGTCACCTGAATTTAGTAATGCCTTTTATGTTACACAACTTAGCACTTTCCAGAAACAAAAACTCTCTCCTTGAAA TAATAGAGTTTTTATCTACCAAAGATATGCTAGTGTCTCATTTCAAAGGCTGCTTTTTCCAGCTTACATTTTATAT ACTTACTCACTTGAAGTTTCTAAATATTCTTGTAATTTTAAAACTATCTCAGATTTACTGAGGTTTATCTTCTGGT GGTAGATTATCCATAAGAAGAGTGATGTGCCAGAATCACTCTGGGATCCTTGTCTGACAAGATTCAAAGGACTAAA TTTAATTCAGTCATGAACACTGCCAATTACCGTTTATGGGTAGACATCTTTGGAAATTTCCACAAGGTCAGACATT CGCAACTATCCCTTCTACATGTCCACACGTATACTCCAACACTTTATTAGGCATCTGATTAGTTTGGAAAGTATGC CTCCATCTGAATTAGTCCAGTGTGGCTTAGAGTTGGTACAACATTCTCACAGAATTTCCTAATTTTGTAGGTTCAG CCTGATAACCACTGGAGTTCTTTGGTCCTCATTAAATAGCTTTCTTCACACATTGCTCTGCCTGTTACACATATGA TGAACACTGCTTTTTAGACTTCATTAGGAATTTAGGACTGCATCTTGACAACTGAGCCTATTCTACTATATGTACA

## FIG. 4B

ATACCTAGCCCATAATAGGTATACAATACACATTTGGTAAAACTAATTTTCAACCAATGACATGTATTTTTCAACT AGTAACCTAGAAATGTTTCACTTAAAATCTGAGAACTGGTTACACTACAAGTTACCTTGGAGATTCATATGAAA ACGCAAACTTAGCTATTTGATTGTATTCACTGGGACTTAAGAATGCGCCTGAATAATTGTGAGTTCGATTTGTTCT GGCAGGCTAATGACCATTTCCAGTAAAGTGAATAGAGGTCAGAAGTCGTATAAAAGAGGTGTTGTCAGAACACCGT TGAGATTACATAGGTGAACAACTATTTTTAAGCAACTTTATTTGTGTAGTGACAAAGCATCCCAATGCAGGCTGAA ATGTTTCATCACATCTCTGGATCTCTATTTTGTGCAGACATTGAAAAAATTGTTCATATTATTTCCATGTTATC CATTAGTCGCCTTCACAACTGATAAAGATCACTGAAGTCAAATTGATTTTTGCTATAATCTTCAATCTACCTATAT TTCACTTAGACAGCTTGGAGACAAGAAATTACCCAAAAGTAAGGTGAGGAGGATAGGCAAAAAAGAGCAGAAAGATG TGAATGGACATTGTTGAGAAATGTGATAGGAAAACAATCATAGATAAAGGATTTCCAAGCAACAGAGCATATCCAG ATGAGGTAGGATGGGATAAACTCTTATTGAACCAATCTTCACCAATTTTGTTTT<u>TCTTTTGCAGA</u>GCAAGCTAGGA CCTGCCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGAAGACCTCACCAAAATTAACAAAACTGAG **ATATGTTCCCAGTTGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATTTCA** 

FIG. 5



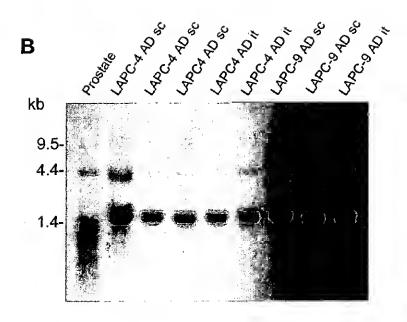


FIG. 6

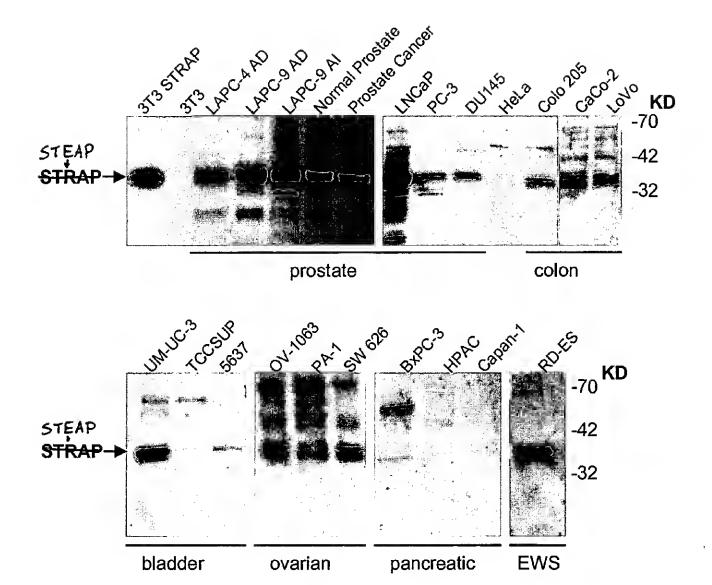
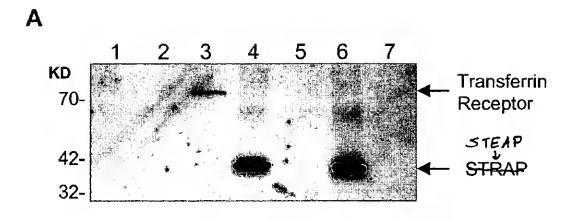
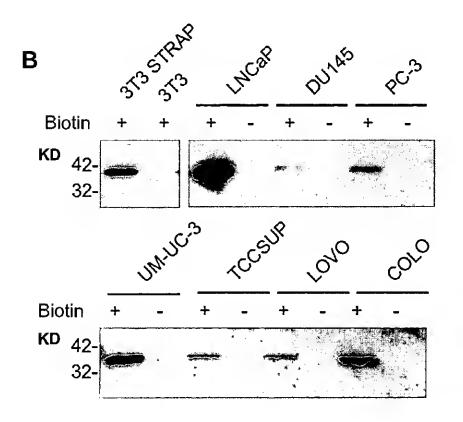


FIG. 7





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											GGC	CCT	CGG	CGC	CAC	AAG	CTG	TCC
	<b>-</b>																	
						73						91						
												AGC						
•			118			127						 145						
(	CTC	CTT										GCT						
												199						217
(	GCT	GGA	GTG	CGA	CCG	CCA	CGG	CAG	CCA	CCC	TGC	AAC	CGC	CAG	TCG	GAG	GTG	CAG
•			226									 253						
-	rcc	GTA										GGA						
			280			289			298			307			316			325
												GGC						
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1	חיד∆	СТТ										GAA				ATG		
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,	rtg	ACC		CGA	СТТ							GTG						
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	P	ĸ	F									V						
															•			·
			604			613												649
(	JAT	GCT	CTC	ACA	AAA	ACA	AAT	ATA	ATA	TTT	GTT	GCT	ATA	CAC	AGA	GAA	CAT	TAT
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			658			667												
7	ACC	TCC	CTG	TGG	GAC	CTG	AGA		CTG	CTT		GGT		ATC	CTG	ATT	GAT	GTG
-																		
	T	S	L	W	D	Г	R	н	L	L	V	G	K	I	Ь	Ι	D	V
			712			721			730			739			748			757
	\CC	דממ		ATG	AGG		AAC	CAG			GAA						•	GCT
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TCA	TTA	766 TTC	CCA	GAT		TTG								802 GTC		GCT	811 TGG
 s		 F	 P	D	 s					 G	 F	 N	 V	 V	 S	 A	 W
GCA	CTT	820 CAG	TTA	GGA	829 CCT		GAT	838 GCC	AGC	CGG		GTT		856 ATA		AGC	8 65 AAC
 A				 G	 P			A '	 s	 R	 Ω	 V		 I		<b>-</b> S	
AAT	ATT	874 CAA	GCG	CGA	883 CAA		GTT			CTT	901 GCC	CGC	CAG	910 TTG		TTC	919 ATT
N	I	Q	A	R	Q	Q	V.	I	E	L.	A	R	Q	L	N	F	I
ccc	ATT	928 GAC	TTG	GGA	937 TCC	TTA	TCA	946 TCA	GCC	AGA	955 GAG	ATT	GAA	964 AAT	TTA	ccc	973 CTA
P	I	D	L	G	s	L	s	S	A	R.	E	I	E	N	L	P	<u>L</u>
CGA	CTC	982 TTT	ACT	CTC	991 TGG									1018 AGC			1027 ACA
R	L	F	T	L	W	R	G	P	V	v	V	A	I	S	L	A	T
TTT		1036 TTC		TAT							1063 ATT			1072 TAT		-	1081 AAC
F	F	F	L	Y	S	F	V	R	D	V	I	H	P	Y	A.	R	N
-		1090 AGT	CAC		1099				מידמ					126			L135
CAA					1AC		A11				A11				ACC	11A	CCT
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Q	Q :	 S 1144	D	 F	 Y 1153	к	I	P. 1162	ı	E 1	I 1 171	<u>v</u>	 N		T		<u>P</u> 1189
Q ATA	Q GTT	S 1144 GCC	D ATT	F	Y 1153 TTG	K CTC	TCC	P 1162 CTA	I GTA	E TAC	I 171 CTT	v GCA	N GGT	K 180	T	L GCA	P 1189 GCT
Q ATA	Q GTT  v	S 1144 GCC A	D ATT	ACT	Y 1153 TTG L	K CTC  L	TCC  S	P 1162 CTA  L	GTA	E TAC Y	I 171 CTT  L	gca 	N GGT G	K 180 CTT	T CTG	GCA	P 1189 GCT  A
Q ATA	GTT V	S 1144 GCC  A 1198 CAA	ATT I CTT	ACT T	Y 1153 TTG  L 1207 TAC	CTC L GGC	TCC  s	P 1162 CTA  L 1216 AAG	GTA V TAT	TAC Y AGG	I L CTT  L L 225 AGA	GCA A TTT	ggt GCA	K 1180 CTT  L	T CTG	GCA	P 1189 GCT  A 1243 GAA
ATA I GCT A	Q GTT  V TAT  Y	S 1144 GCC A 1198 CAA Q 1252	ATT I CTT L	ACT T TAT Y	Y 1153 TTG L 1207 TAC Y	CTC L GGC G	TCC S ACC T	P 1162 CTA  L 1216 AAG  K	GTA V TAT Y	E TAC Y AGG R	I 171 CTT  L 1225 AGA  R	GCA A TTT	N GGT G CCA	K 180 CTT L 234 CCT P	T CTG	GCA TTG	P 1189 GCT ———————————————————————————————————
Q ATA I GCT A	Q GTT V TAT Y TGG	S 1144 GCC A 1198 CAA Q 1252 TTA	ATT I CTT L CAG	ACT TAT Y TGT	Y 1153 TTG L 1207 TAC Y	CTC L GGC G	TCC S ACC T CAG	P 1162 CTA  L 1216 AAG  K	GTA V TAT Y GGA	E TAC Y AGG R	I 171 CTT L 225 AGA R 1279 CTA	GCA A TTT F	GGT G CCA P	180 CTT  L 1234 CCT  P	T CTG	GCA TTG GCT	P I189 GCT A I243 GAA  E I297 ATG
Q ATA I GCT A ACC	GTT V TAT Y TGG W	S 1144 GCC A 1198 CAA Q 1252 TTA L	ATT I CTT L CAG	F ACT TAT Y TGT	Y 1153 TTG L 1207 TAC Y 1261 AGA R	CTC L GGC G	TCC S ACC T CAG	P 1162 CTA  L 1216 AAG  K 1270 CTT	I GTA V TAT Y GGA G	E TAC Y STA L	I 171 CTT L 1225 AGA R 1279 CTA L 1333	GCA A TTT F AGT	GGT G CCA P TTTT F	180 CTT  L 1234 CCT  P	T CTG	GCA TTG L GCT A	P 1189 GCT A 1243 GAA  ATG 1351
Q ATA I GCT A ACC	O GTT V TAT Y TGG W CAT	1144 GCC  A 1198 CAA  Q 1252 TTA  L	ATT I CTT L CAG	TAT Y TGT C	Y 1153 TTG L 1207 TAC Y 1261 AGA R	GGC G AAA K CTC	TCC S ACC T CAG Q TGC	P 1162 CTA  L 1216 AAG  K 1270 CTT  L	TAT Y GGA CCG	E TAC	I 171 CTT L 225 AGA R 279 CTA L 333 AGA	GCA A TTT F AGT S	GGT G CCA TTTT F TCA	K 180 CTT L 234 CCT P 288 TTC F	T CTG	GCA TTG L GCT A	P 1189 GCT A 1243 GAA  ATG 1351 TTG
Q ATA I GCT A ACC T GTC V	O GTT V TAT Y TGG W CAT H	1144 GCC  A 1198 CAA  Q 1252 TTA  L 1306 GTT  V	ATT L CAG Q GCC A	TAT TAC TAC TAC TAC TAC	1153 TTG  L 1207 TAC  Y 1261 AGA  R 1315 AGC  S	GGC G AAA K CTC L CAG CAG	TCC S ACC T CAG Q CAG CAG	P 1162 CTA  L 1216 AAG  K 1270 CTT  L 1324 TTA  L	TAT Y GGA CCG P	TAC TAC TAC TAC TAC TAC AGG AGG A TTA TTA ATG ATG ATG	I 171 CTT L 225 AGA R 279 CTA L 333 AGA R 387 AAT	GCA A TTT F AGT S AGG R ATT	GGT GCA TTTT TCA S GAA	180 CTT L 234 CCT P 288 TTC F 342 GAG E	TGG W TTC F AGA R	GCA TTG TAT TGG	P 189 GCT A A GAA ATG L 405 AAT
Q ATA I GCT A ACC T GTC V	O GTT V TAT Y TGG W CAT H	1144 GCC  A 1198 CAA  Q 1252 TTA  L 1306 GTT  V	ATT L CAG Q GCC A	TAT TAC TAC TAC TAC TAC	1153 TTG  L 1207 TAC  Y 1261 AGA  R 1315 AGC  S	GGC G AAA K CTC L CAG CAG	TCC S ACC T CAG Q CAG CAG	P 1162 CTA  L 1216 AAG  K 1270 CTT  L 1324 TTA  L	TAT Y GGA CCG P	TAC TAC TAC TAC TAC TAC AGG AGG A TTA TTA ATG ATG ATG	I 171 CTT L 225 AGA R 279 CTA L 333 AGA R 387 AAT	GCA A TTT F AGT S AGG R ATT	GGT GCA TTTT TCA S GAA	180 CTT  L 1234 CCT  P 1288 TTC  F	TGG W TTC F AGA R	GCA TTG TAT TGG	P 189 GCT A 1243 GAA  ATG L 1405 AAT
Q ATA  I  GCT A  ACC T  GTC V  TTT F	TAT TGG W CAT H	1144 GCC  A 1198 CAA  Q 1252 TTA  L 1306 GTT  V	D ATT I CTT L CAG Q GCC A A ATG	TAT Y TAC TAC TAC TAC A	Y 1153 TTG L 1207 TAC Y 1261 AGA R 1315 AGC S 1369 TAT Y	GGC G AAA K CTC L CAG Q ATT	TCC S ACC T CAG Q CAG CAG Q 1	P 1162 CTA  L 1216 AAG  K 1270 CTT  L 1324 TTA  L	TAT Y GGA CCG P CAT	E TAC TAC TAC TAC TAC AGG A TTA ATG ATG ATG ATG ATG ATG ATG A	I 171 CTT L 225 AGA R 279 CTA L 333 AGA R AAT N L 441 TCC	GCA TTT F AGT S AGG R ATT I	GGT G CCA P TTT TCA S GAA E	180 CTT  L 234 CCT  P 288 TTC  F 342 GAG  N	TGG W TTC F AGA R TCT S ATG	GCA TTG TAT TGG Y	P 189 GCT A 1243 GAA  ATG 1351 TTG AAT N 1459 CTT

		1468		•	1477		:	1486			1495			<sub>-</sub> 504			1513
GGC	TTA	CTT	TCC	CTC	CTG	GCA	GTC	ACT	TCT	ATC	CCT	TCA	G1 3	AGC	AAT	GCT	TTA
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G	L	L	Ş	L	L	A	v	T	S	I	P	_\$_	V	S	N	Α	Ļ
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		1522												1558			1567
AAC	TGG	AGA	GAA	TTC	AGT					ACA	CTT	GGA	TAT	GTC	GCT	CTG	CTC
N	W	R	E	F.	S	<u>F.</u>	<u> I</u>	Q	\$	T	L	G	Y	v	A	L	<u> </u>
		1576			1585			1501			1603			1610			1.601
2002			TTTC											1612 TTT	~~~		1621
AIA	AGI	ACI		CAI						166	AAA	CGA	GCI	TTT	GAG	GAA	GAG
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		1630		1	1639			1648			1657			1666			1675
TAC	TAC	AGA												GTT			
Y	Y	R	F	Y	T	P	P	N	F	v	L	A	L	v	L	P	S
		1684		1			:	1702			1711			1720			1729
ATT	GTA	ATT	CTG	GAT	CTT	TTG	CAG	CTT	TGC	AGA	TAC	CCA	GAC	TGA	GCT	GGA	ACT
<u> </u>	V	<u>_</u>	_ь	ъ	_ <u>+</u> _		Ψ	Ъ	<u> </u>	R	Y	P	D	*			
		1738		-	17/7			1756			1765			1774			1702
GGA														GCC			
	:	1792												1828			
CCT	CAG	CTG	TCC	TTG	CAG	TTA	GGT	GTA	CAT	GTG	ACT	GAG	TGT	TGG	CCA		
	•	1846		1	1855		- :	1864			1873			1882		:	1891
TGA	AGT	CTC	CTC	AAA	GGA	AGG	CAG	CAT	GTG	TCC	TTT	TTC	ATC	CCT	TCA	TCT	TGC
														 1936			
		1900		3	1909		1	1918			1927			1936		1	L945
TGC	TGG	GAT	TGT	GGA	TAT	AAC	AGG	AGC	CCT	GGC	AGC			CAG			
000	_	L954		C2C										1990	7 AM		L999
														TTG			
		2008												2044			2053
СТА		-								_				GGG		_	
	2	2062		2	2071		2	2080			2089			2098		2	2107
TGA	AGT	GAA				TTT	CTG	CCC	TTC	AGT	TCT	TTA		TGA			TTA
		2116												2152			
														AAA			
														2206			
														ATT			
														2260			
			GCC	<b>ጥጥ</b> ር	ATC	ттт	САТ	TAG	ΔΤΔ	ւրսեր	TCT	Σጥሮ	TCC	TTG	CAA	ጥልጥ	2 0 3 Δጥጥ
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ATC.														TAA			
	2	2332		2	2341		2	2350		2	2359			2368		2	2377
TAT	TGC	TAT	CAA	ATT	ACA	CAC	CAT	GTT	TTC	TAT	CAT	TCT	CAT	AGA	TCT	GCC	TTA
														2422			2431
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				AAA				o .									

#### THUS STEADED FIRST STILL STORE STORES

## FIG. 10A-1

(SEQ ID NO: 7)

- 1 CGAAACTTCC CTCTACCCGC CCGGCCCGCG GCGCGCACCG TTGGCGCTGG ACGCTTCCTC
  GCTTTGAAGG GAGATGGGCG GGCCGGGCGC CGCGCGTGGC AACCGCGACC TGCGAAGGAG
- (SEQ IN NO:8)→M E K T C I D A L P L T
  61 CTTGGAAGCG CCTCTCCTC AGTTATGGAG AAAACTTGTA TAGATGCACT TCCTCTTACT
  GAACCTTCGC GGAGAGGGAG TCAATACCTC TTTTGAACAT ATCTACGTGA AGGAGAATGA
- M N S S E K Q E T V C I F G T G D F G R 121 ATGAATTCTT CAGAAAAGCA AGAGACTGTA TGTATTTTTG GAACTGGTGA TTTTGGAAGA TACTTAAGAA GTCTTTTCGT TCTCTGACAT ACATAAAAAC CTTGACCACT AAAACCTTCT
- S L G L K M L Q C G Y S V V F G S R N P

  181 TCACTGGGAT TGAAAATGCT CCAGTGTGGT TATTCTGTTG TTTTTGGAAG TCGAAACCCC
  AGTGACCCTA ACTTTTACGA GGTCACACCA ATAAGACAAC AAAAACCTTC AGCTTTGGGG
- Q K T T L L P S G A E V L S Y S E A A K 241 CAGAAGACCA CCCTACTGCC CAGTGGTGCA GAAGTCTTGA GCTATTCAGA AGCAGCCAAG GTCTTCTGGT GGGATGACGG GTCACCACGT CTTCAGAACT CGATAAGTCT TCGTCGGTTC
- K S G I I I I A I H R E H Y D F L T E L

  301 AAGTCTGGCA TCATAATCAT AGCAATCCAC AGAGAGCATT ATGATTTTCT CACAGAATTA
   TTCAGACCGT AGTATTAGTA TCGTTAGGTG TCTCTCGTAA TACTAAAAGA GTGTCTTAAT
- T E V L N G K I L V D I S N N L K I N Q

  361 ACTGAGGTTC TCAATGGAAA AATATTGGTA GACATCAGCA ACAACCTCAA AATCAATCAA
  TGACTCCAAG AGTTACCTTT TTATAACCAT CTGTAGTCGT TGTTGGAGTT TTAGTTAGTT
- Y P E S N A E Y L A H L V P G A H V V K
  421 TATCCAGAAT CTAATGCAGA GTACCTTGCT CATTTGGTGC CAGGAGCCCA CGTGGTAAAA
  ATAGGTCTTA GATTACGTCT CATGGAACGA GTAAACCACG GTCCTCGGGT GCACCATTTT
- A F N T I S A W A L Q S G A L D A S R Q
  481 GCATTTAACA CCATCTCAGC CTGGGCTCTC CAGTCAGGAG CACTGGATGC AAGTCGGCAG
  CGTAAATTGT GGTAGAGTCG GACCCGAGAG GTCAGTCCTC GTGACCTACG TTCAGCCGTC
- V F V C G N D S K A K Q R V M D I V R N 541 GTGTTTGTGT GTGGAAATGA CAGCAAAGCC AAGCAAAGAG TGATGGATAT TGTTCGTAAT CACAAACACA CACCTTTACT GTCGTTTCGG TTCGTTTCTC ACTACCTATA ACAAGCATTA
- L G L T P M D Q G S L M A A K E I E K Y 601 CTTGGACTTA CTCCAATGGA TCAAGGATCA CTCATGGCAG CCAAAGAAAT TGAAAAGTAC GAACCTGAAT GAGGTTACCT AGTTCCTAGT GAGTACCGTC GGTTTCTTTA ACTTTTCATG
- P L Q L F P M W R F P F Y L S A V L C V
  661 CCCCTGCAGC TATTTCCAAT GTGGAGGTTC CCCTTCTATT TGTCTGCTGT GCTGTGTGTC
  GGGGACGTCG ATAAAGGTTA CACCTCCAAG GGGAAGATAA ACAGACGACA CGACACACAC
- F L F F Y C V I R D V I Y P Y V Y E K K
  721 TTCTTGTTT TCTATTGTGT TATAAGAGAC GTAATCTACC CTTATGTTTA TGAAAAGAAA
  AAGAACAAAA AGATAACACA ATATTCTCTG CATTAGATGG GAATACAAAT ACTTTTCTTT

DNTF & MAISIPNRI PPITAL 781 GATAATACAT TTCGTATGGC TATTTCCATT CCAAATCGTA TCTTTCCAAT AACAGCACTT CTATTATGTA AAGCATACCG ATAAAGGTAA GGTTTAGCAT AGAAAGGTTA TTGTCGTGAA TLLALVY L PG V I A A I L Q L Y R 841 ACACTGCTTG CTTTGGTTTA CCTCCCTGGT GTTATTGCTG CCATTCTACA ACTGTACCGA TGTGACGAAC GAAACCAAAT GGAGGGACCA CAATAACGAC GGTAAGATGT TGACATGGCT G T K Y R R F P D W L D H W M L C R K O 901 GGCACAAAAT ACCGTCGATT CCCAGACTGG CTTGACCACT GGATGCTTTG CCGAAAGCAG CCGTGTTTTA TGGCAGCTAA GGGTCTGACC GAACTGGTGA CCTACGAAAC GGCTTTCGTC LGLVALGFAFLHVL YTL 961 CTTGGCTTGG TAGCTCTGGG ATTTGCCTTC CTTCATGTCC TCTACACACT TGTGATTCCT GAACCGAACC ATCGAGACCC TAAACGGAAG GAAGTACAGG AGATGTGTGA ACACTAAGGA IRYYVRW RLG NLTV T Q A I L K 1021 ATTCGATATT ATGTACGATG GAGATTGGGA AACTTAACCG TTACCCAGGC AATACTCAAG TAAGCTATAA TACATGCTAC CTCTAACCCT TTGAATTGGC AATGGGTCCG TTATGAGTTC KENPFSTSSAWLSDSYVALG 1081 AAGGAGAATC CATTTAGCAC CTCCTCAGCC TGGCTCAGTG ATTCATATGT GGCTTTGGGA TTCCTCTTAG GTAAATCGTG GAGGAGTCGG ACCGAGTCAC TAAGTATACA CCGAAACCCT I L G F F L F V L L G I T S L P S V S N 1141 ATACTTGGGT TTTTTCTGTT TGTACTCTTG GGAATCACTT CTTTGCCATC TGTTAGCAAT TATGAACCCA AAAAAGACAA ACATGAGAAC CCTTAGTGAA GAAACGGTAG ACAATCGTTA A V N W R E F 'R F V Q S K L G Y L T L I 1201 GCAGTCAACT GGAGAGAGTT CCGATTTGTC CAGTCCAAAC TGGGTTATTT GACCCTGATC CGTCAGTTGA CCTCTCTCAA GGCTAAACAG GTCAGGTTTG ACCCAATAAA CTGGGACTAG L C T A H T L V Y G G K R F L S P S N L 1261 TTGTGTACAG CCCACACCCT GGTGTACGGT GGGAAGAGAT TCCTCAGCCC TTCAAATCTC AACACATGTC GGGTGTGGGA CCACATGCCA CCCTTCTCTA AGGAGTCGGG AAGTTTAGAG RWYL PAA Y V L G L I I P C T V L V 1321 AGATGGTATC TTCCTGCAGC CTACGTGTTA GGGCTTATCA TTCCTTGCAC TGTGCTGGTG TCTACCATAG AAGGACGTCG GATGCACAAT CCCGAATAGT AAGGAACGTG ACACGACCAC I K F V L I M P C V D N T L T R I 1381 ATCAAGTTTG TCCTAATCAT GCCATGTGTA GACAACACCC TTACAAGGAT CCGCCAGGGC TAGTTCAAAC AGGATTAGTA CGGTACACAT CTGTTGTGGG AATGTTCCTA GGCGGTCCCG WERNSKH 1441 TGGGAAAGGA ACTCAAAACA CTAGAAAAAG CATTGAATGG AAAATCAATA TTTAAAACAA ACCCTTTCCT TGAGTTTTGT GATCTTTTTC GTAACTTACC TTTTAGTTAT AAATTTTGTT 1501 AGTTCAATTT AGCTGGATTT CTGAACTATG GTTTTGAATG TTTAAAGAAG AATGATGGGT TCAAGTTAAA TCGACCTAAA GACTTGATAC CAAAACTTAC AAATTTCTTC TTACTACCCA 1561 ACAGTTAGGA AAGTTTTTTT CTTACACCGT GACTGAGGGA AACATTGCTT GTCTTTGAGA TGTCAATCCT TTCAAAAAAA GAATGTGGCA CTGACTCCCT TTGTAACGAA CAGAAACTCT 1621 AATTGACTGA CATACTGGAA GAGAACACCA TTTTATCTCA GGTTAGTGAA GAATCAGTGC TTAACTGACT GTATGACCTT CTCTTGTGGT AAAATAGAGT CCAATCACTT CTTAGTCACG

1681				G IGAGACT CTAACTCTGA	
1741				GACCTAATGT CTGGATTACA	
1801				TGAGTTAAGT ACTCAATTCA	
1861				TATCTGAGGA ATAGACTCCT	
1921				GAAGTAAAGG CTTCATTTCC	
1981				TGCTTTTCTT ACGAAAAGAA	
2041	=			ACAATTGATT TGTTAACTAA	
2101			 	TTCTTCCTCT AAGAAGGAGA	
2161				TGGATTTCAC ACCTAAAGTG	
2221	=		· ·	AGTTCAAAGA TCAAGTTTCT	
2281				ATTAGGTTAA TAATCCAATT	
2341				TGCTCAATAT ACGAGTTATA	
2401		<del>-</del>	 	GTCTTAGTCT CAGAATCAGA	ATTATAATTG TAATATTAAC
2461	TAAGGAGTAA ATTCCTCATT				ATAGATGATC TATCTACTAG
2521	GAAAATTACG CTTTTAATGC				GTGAAATTTG CACTTTAAAC
2581					TGTGCTGATA ACACGACTAT
2641				TAGCTCAAGC ATCGAGTTCG	AATGAGCTAA TTACTCGATT
2701	AAGGAGCCTT TTCCTCGGAA			TAAAAGGCAC ATTTTCCGTG	•
2761					TAACATATTA ATTGTATAAT

2821		I. ACAAAAA ATATGTTTTT				
2881		AAACTTTTTA TTTGAAAAAT				
2941		GTTTTTCTAA CAAAAAGATT				
3001		AGTCTTGCTC TCAGAACGAG				
3061		CTCCTCCCAG GAGGAGGGTC				
3121		ATGTGCCACT TACACGGTGA				<del>-</del>
3181		GGTCAGGCTG CCAGTCCGAC	•			
3241		ATATTTTCTT TATAAAAGAA				
3301	= =	TATTAAACAT ATAATTTGTA				
3361	=	TTTGCACTGA AAACGTGACT				<del>-</del>
3421		GGATGAGGGT CCTACTCCCA				
3481		TTATTTATAA AATAAATATT				
3541		AACCCAAGCA TTGGGTTCGT			•	
3601	ATACGGTGCT TATGCCACGA	GACCCTACAG CTGGGATGTC	= =			
3661	TGTTATGCAA ACAATACGTT	AACAGTTAGG TTGTCAATCC				-
3721	TTGATTAAAG AACTAATTTC	TTTAGGTACC AAATCCATGG				
3781		AAAGAAGAGA TTTCTTCTCT				
3841	AGAAAATGCC TCTTTTACGG	ATCCATAGGT TAGGTATCCA			_	
3901	AGCCTAGTAA TCGGATCATT	AAATGCTCTA TTTACGAGAT				
•			FIG. 10	A-4		

3961	GAGCACTCTG	A. JTTTTGG	CATAATAGCT	GCATTTCCAG	Ac . IGACCTT	TGGCCCCAAC
	CTCGTGAGAC	TACCAAAACC	GTATTATCGA	CGTAAAGGTC	TGGACTGGAA	ACCGGGGTTG
- 4021	CACAAGTGCT	CCAAGCCCCA	CCAGCTGACC	AAAGAAAGCC	CAAGTTCTCC	TTCTGTCCTT
	GTGTTCACGA	GGTTCGGGGT	GGTCGACTGG	TTTCTTTCGG	GTTCAAGAGG	AAGACAGGAA
4081					ACCATATTAA	
	GGGTGTTGGA	GGGACGAGGG	TTTTGATACT	TTAATTAAAC	TGGTATAATT	GTGTCGACTG
4141					AGATGAAAAT	
	AGGAGGTCAA	ATGAATTCCA	TCTTTCTTAC	TCAAATGTTG	TCTACTTTTA	TTCACGAAAC
4201					ATTTAAAAAA	
	CCGCTTGACA	TAAGGAAAAT	TGTCTAGGTT	TGATAAAATG	TAAATTTTTT	TTTCAATTTG
4261	TAAACTTCTT	TACTGCTGAT	ATGTTTCCTG	TATTCTAGAA	AAATTTTTAC	ACTTTCACAT
	ATTTGAAGAA	ATGACGACTA	TACAAAGGAC	ATAAGATCTT	TTTAAAAATG	TGAAAGTGTA
321	TATTTTTGTA	ĈACTTTCCCC	ATGTTAAGGG	ATGATGGCTT	TTATAAATGT	GTATTCATTA
	ATAAAAACAT	GTGAAAGGGG	TACAATTCCC	TACTACCGAA	AATATTTACA	CATAAGTAAT
1381	AATGTTACTT	TAAAAATAAA	AAAAAAAAA	AAAAAAAA	AAAAAAA	
	TTACAATGAA	ATTTTTTTT	TTTTTTTTTT	TTTTTTTTT	TTTTTTTT	_

FIG. 10A-5

## FIG. 10B

### STEAP-2, AA508880 (NCI CGAP Pr6)

### STEAP-2, 98P4B6 SSH fragment

TTTGCAGCTTTGCAGATACCCAGACTGAGCTGGAACTGGAATTTGTCTTCCTATTGACTCTTCTTTAAAAGCG GCTGCCCATTACATTCCTCAGCTGTCCTTGCAGTTAGGTGTACATGTGACTGAGTGTTGGCCAGTGAGATGAAGTC TCCTCAAAGGAAGGCAGCATGTGTCCTTTTT (SEQPACO:10)

#### STEAP-3, AI139607 (testis EST)

(SEQ IS NO:11)

#### STEAP 4, R80991 (placental EST)

87 75 0	177 165 36 0	266 254 125 0	356 344 215 31
76 VVDATHHEDALTATN GAENLSYSENAKASG	166 ROVET BSINIORRO ROVEVEGINDS KAKOR EDDEL - HKDTGETS	270 DEDVNKTEPIVATTI ESHPNRIFPITALTI ULVINKVERNSETTI	346 HANI ENSWNEREVWR ILKENPFSTSSAML QONKEDANIEHDWN WPXKSHLMVKERWR
61 IGSRNEKFASEFFPH FGSRNEOKTT-LLPS	151 165 VVSAWALIGL PLDAE TISAWALIGS ALLDAE QEELMEWE PRINIE	255 REYARNOGSDEYKIR YPYVYEKKDNIFRMA HELAISHGOVEYKIR	331 REERYLFINMAYOOV YYVRWRIGNITYTÖA REYKYKILIMAYOOV AAXATTWSTWOSSRS
46 KETTIRLIRGGYHW REIGLKMLOGGYSKY	136 LASLFBDSLIVAGEN LAHLVEGAHVNAAEN	226 HATRFELYSFVKDV HCVFLFFXCVIKDV IASLTRINTLIREV	316 FANVHVAYSICLENK FANTHVATIVIEL FAVLHAIKSISYEME
31 45 ARKVINGVIĞSÜDEA -KQEİNCIFĞIĞDEG	NIMETROYPESNAEY	211 RIETLWRGEVVVRIS OLFFWWRFFYLSRV RUEBOWHLHIKIRNI	301 TÄLOCKKÖLGLESFR HWMLCKKÖLGIVALG KWMLTRKÖRGLISFR
16 TGFENGINGIKD TGIDALHLTMNSSE-	106 DERILEVEKTETED 120 ETTEVENGKETEVETE	196 210 LUGSISSARETENLER QUESTMANKETEKYET ADEFDCPSELQH-TQ	300 LYYGTKYRRPPWIE LYRGTKYRRPPOWIE HWGTKYKKPPWIT
STEAP2 MESISMMGSPKSLSE STEAP3MEK STEAP1	105 ETEVATERENTISEW ETITATERENTEETT	MIELAROENE-IBIN 195 1 WINDIVENICE-TEMP OLKRPVLEHHOTAH F	271 285 BSLVYTAGLLAAAYO IALVYTAGVIAATU LALVYTEGVIAATVO
2 STEAP2 3 STEAP3 4 STEAP1 5 STEAP4	2 STEAP2 3 STEAP3 4 STEAP1 5 STEAP4	2 STEAP2 3 STEAP3 4 STEAP1 5 STEAP4	2 STEAP2 3 STEAP3 4 STEAP1 5 STEAP4

# FIG. 11A-2

445 434 305 120				
436  VILLATOLIA SIVALD  VALCHII PCTALVIR  MIAVELITY TATER  MIXTELVE - CARSSW				•
A21 RAPERENTRFTTPEN RFLSPENLRWYIDEA KWIDI KOFWYTPET RAFRESREKETIPET				
406 ALDISTFRATIVEDENT THILCTARTHVEGEN STUTIONIHALIFANI AXVISTIATITYS				
405 NWREFERIOGILGYV NWREFREVOSKLGYL TWREFRYTOSKLGIL NWREFRYOSKLGIV		2017 2017 2017	CSQL 339	133
390 SELAVISIDESVENAL VEIGTESTENAV ALIAVISIDETANEL SELAVISIDETANEL	466 480	ROGWERNSKH	RHGWEDVTRINKTEI	
361 2 STEAP2 IEMŢISFGIMSLGHI 3 STEAP3 SDSKVAHGINGFFÜF 4 STEAP1 MRITVSÜĞIVÜNIN 5 STEAP4 MRIXLSÜĞVÜALÖTÜ	451 11.07/CPVBR	3 STEAP3 FVIIMPGVDNTLTRI ROGWERI	SILFUPCLEKKILKE	5 STEAP4 AKADEXLECTOPX
2 STEAP2 3 STEAP3 4 STEAP1 5 STEAP4	CONTRACTOR C	3 STEAP3	4 STEAP1	5 STEAP4

# FIG. 11B

STRAP-1	67	LFP	QWH	LP:	IKI.	AΑ	II	151	T	T.	T.	LLi	RE'	VI	HР	L.	TS	HQ	QY	FΥ	KI	Ρ.	$\Gamma$	VI.	NK	VL	PM	VS:	ΙΤΙ	L
STRAP-2	208	LFT	LWR	GP۱	777	AT.	SL	ATI	E.	L	YS:	FVI	RD	VI	ΗP	ΥA	RN	QQ	SD	FY	KI	P	EE:	IV	NK:	TL	PI	VA.	ITI	L
		**	*	*		*	1	k	1	k * 1	*	•	*	* *	* *	*		*		* *	* *	*	k		* *	*	* ;	*	***	*
STRAP-1	127	ALV	YLP	GV.	<b>LA</b> A	ΙV	QLE	INC	TF	(YF	KK.	FP	HW:	LD	KW	ML	TR	KQ	FG	ĿI	SE	ΈΊ	FA	VI.	HA.	ΙY	SL	SY:	PMP	ŁR
STRAP-2	268	SLV	YLA	GLI	LAA	ΑY	QL:	YY	TI	<b>CYF</b>	RR:	FP!	PW:	LΕ	TW	LQ	CR	ΚQ	LG	ĹΙ	SE	Έl	TA!	MV.	HV	ΑY	SL	CL!	PMP	R
			**																										***	
STRAP-1	187	SYR	YKL	LN	/AY	ΟO.	VQQ	ONE	ŒI	OAV	VI)	ЕНІ	DVI	ΝR	ME	ΙY	vs	LG	IV	GI	AI	L	L)	LA'	VI:	SI	PSY	VS!	DSI	T
STRAP-2	328	SER	YLF	LN	1AY	00	VH	AN]	E	ISV	٧N	EEI	EVI	٧R	ΙE	ΜY	IS	FG	ΙM	SI	GI	L	3L3	LA	VT:	SI	PS V	VS1	NAI	N
		* *			**														*								**			
STRAP-1	247	WRE	FHY	IQS	SKL	GI	VSI	LLI	.GI	CIF	IA:	LI	FAI	WN	KW	ΊD	IK	QF	VW	ΥΊ	'PE	TI	·M:	IA'	VF:	LP	IV	VL:	I	
STRAP-2		WRE																												
		***	*	**	+ +	<del>-</del>	* +	. *	,		. ,	* *	,	k .						* *	**			*			,	*	_	

# FIG. 11C

STEAP1	66	ELFPQV	VHLPIF	IIAAII	ASLTFL	YTLL	REVIE	IPLAT	CSHQQ	YFYKI	[PILV	INK	VLP	MVS	ITL
STEAP3	195	QLFPMV		'LSAVL *	CVFLFF *		RDVIY * **	(PYV) *	ÆKKD	NTFR	4AIS] *	PNR *	IFP *	ITA	LTL **
STEAP1	126	LALVYI	LPGVIA	AIVQL	HNGTKY	KKFPI	HWLDK	CWMLT	rkQf	GLLSE	FFAV	/LHA	IYS	LSY	PMR
STEAP3	255				YRGTKY: ****							LHV **			
STEAPİ	186	RSYRYI	CLLNWA	YQQVQ	QNKEDA	WIEHI	DVWRM	ŒIYV	/SLGI	VGLAI	CLALI	.AVT	SIP	svsi	DSL
STEAP3	315	YYVRWI *	RLGNLT	VTQAI *	LKKENP:	FSTS	SAWLS *	DSYV **	/ALGI	LGFFI *	LFVLI	GIT *	SLP	SVS! ***	VAN
STEAP1	246	TWREF	IYIQSK	LGIVS	LLLGTI	HALII	FAWNK	WIDI	KQFV	WYTPE	TFMI	AVF	LPI.	VVL:	IFK
STEAP3	375	NWREFF	_		LILCTAI		YGGKR	≀FLSE	SNLR	WYLPA ** *	AYVI	.GLI	IPC' *	TVL' * *	VIK *
STEAP1	306	SILFL	CLRKK	ILKIR	HGWEDV	TK,									

# FIG. 11D

STEAP2	29	RKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGSRNPKFASEFFPHVVDVTHHEDALTKTNI
STEAP3	18	KQETVCIFGTGDFGRSLGLKMLQCGYSVVFGSRNPQ-KTTLLPSGAEVLSYSEAAKKSGI ** * *** **
STEAP2	89	IFVAIHREHYTSLWDLRHLLVGKILIDVSNNMRINQYPESNAEYLASLFPDSLIVKGFNV
STEAP3	77	IIIAIHREHYDFLTELTEVLNGKILVDISNNLKINQYPESNAEYLAHLVPGAHVVKAFNT * ****** * * * **** * ******** * * * *
STEAP2	149	VSAWALQLGPKDASRQVYICSNNIQARQQVIELARQLNFIPIDLGSLSSAREIENLPLRL
STEAP3	137	ISAWALQSGALDASRQVFVCGNDSKAKQRVMDIVRNLGLTPMDQGSLMAAKEIEKYPLQL
STEAP2	209	${\tt FTLWRGPVVVAISLATFFFLYSFVRDVIHPYARNQQSDFYKIPIEIVNKTLPIVAITLLS}$
STEAP3	197.	FPMWRFPFYLSAVLCVFLFFYCVIRDVIYPYVYEKKDNTFRMAISIPNRIFPITALTLLA  * ** *
STEAP2	269	LVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQCRKQLGLLSFFFAMVHVAYSLCLPMRRS
STEAP3	257	LVYLPGVIAAILQLYRGTKYRRFPDWLDHWMLCRKQLGLVALGFAFLHVLYTLVIPIRYY **** * ** *** ****** ** * ****** ** * *
STEAP2	329	ERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALNW
STEAP3	317	VRWRLGNLTVTQAILKKENPFSTSSAWLSDSYVALGILGFFLFVLLGITSLPSVSNAVNW  * * * * * * * * * * * * * * * * * * *
STEAP2	389	REFSFIQSTLGYVALLISTFHVLIYGWKRAFEEEYYRFYTPPNFVLALVLPSIVIL
STEAP3	377	REFRFVQSKLGYLTLILCTAHTLVYGGKRFLSPSNLRWYLPAAYVLGLIIPCTVLV